

SEQUENCE LISTING

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<120> NOVEL GENES AND POLYPEPTIDES FOR THE
 DIAGNOSIS OF GIANT CELL ARTERITIS



RECEIVED

<130> 07419-029001

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<140> 09/484,577

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TECH CENTER 1600/2900

<160> 98

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 682

<212> DNA

<213> Homosapiens

<220>

<223> artificially generated nucleic acid

<400> 1

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ctaaacggag	gatctcacga	acatccgctc	caaccccgac	accacgctcc	ccgcccgtcac	120
gacaggctcg	ctgccttcct	cgcgcaagtt	cttgcataatc	cctgaggccg	cgcccgacat	180
ccgcgttccc	ttgcgcgaga	tcatcctgtc	cgagggcgcc	ggcgagccga	acctgcccgt	240
ctatgacacc	tcggggccct	acaccgatcc	ggccgtgacg	atcgacgtca	acagccgcct	300
gccgcgcaat	cgcctcgcct	gggtcaaggaa	acgcggcgcc	gtcgaggaat	atcaggccgc	360
accatcaagc	cggaggacaa	cggcaatgtc	ggcgcatccc	acgcccggaa	ggcggttcacc	420
ggcaccacaa	gccgctgcgc	gctcgacgg	cacaagatca	cccactcgag	ttcgccgcgc	480
cggcattata	ccaaggagat	gatctacgtc	gccgagcgtg	agaatcttgg	cgcaaggcagc	540
agctgagcgc	gccgaggccg	gctgccgacg	gaagagttt	ggccgcgg	tgccggctta	600
ttacgccgga	atttgtcgca	agagatcgcg	cgccggccat	tatttcctt	aaaattaaca	660
ttgccgagct	tgaaccgatg	aa				682

<210> 2

<211> 92

<212> PRT

<213> Homosapiens

<400> 2

Leu	Pro	Ala	Val	Thr	Thr	Gly	Ser	Leu	Pro	Ser	Ser	Arg	Lys	Phe	Phe
1				5				10				15			
Ala	Ile	Pro	Glu	Ala	Ala	Pro	Asp	Ile	Arg	Val	Pro	Leu	Arg	Glu	Ile
					20			25			30				
Ile	Leu	Ser	Glu	Gly	Ala	Gly	Glu	Pro	Asn	Leu	Pro	Val	Tyr	Asp	Thr
					35			40			45				
Ser	Gly	Pro	Tyr	Thr	Asp	Pro	Ala	Val	Thr	Ile	Asp	Val	Asn	Ser	Gly
					50			55			60				
Leu	Pro	Arg	Asn	Arg	Leu	Ala	Trp	Val	Lys	Glu	Arg	Gly	Gly	Val	Glu
65					70				75			80			
Glu	Tyr	Gln	Ala	Ala	Pro	Ser	Ser	Arg	Arg	Thr	Thr				
					85			90							

<210> 3
<211> 501
<212> DNA
<213> Homosapiens

<220>
<223> Synthetically generated nucleic acid

<400> 3

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aacccgggac gagctggcct tcctgccggc cgcgcctcgaa attgtcgaga cgccgcac	120
tcccaccgcg agactcacgg ccgccttgct tgctgccttgc ttctactgcg ccgtggcg	180
ggcgggtctc ggcaggatcg acatcggtgc ttctgcattcc agaaaagatcg tgccggcg	240
ccgtgtaaag ctgggtcagc cgctcgaggc cggcggtggc cggggccactc atgtccgcg	300
tggccaaacc gtcaaggccg gcgagattct gatecgagctg gatccattcg cgggtgggtgt	360
ggatgtgcg cccccgtcaga gtcacatcac ggtgtcgccg ccccacggat cgccacacca	420
tcttgcac ctttcttcac cgacgagtca ccggcggagtt gccgatattt cgtgatctta	480
tcagaatgcg gcgatgatca t	501

<210> 4
<211> 124
<212> PRT
<213> Homosapiens

<400> 4

Leu Ser Ser Leu Ser Pro Arg Met Lys Ser Ala Arg Glu Val Val Ala	
1 5 10 15	
Val Gly Gly Lys Thr Arg Asp Glu Leu Ala Phe Leu Pro Ala Ala Leu	
20 25 30	
Glu Ile Val Glu Thr Pro Pro Ser Pro Thr Ala Arg Leu Thr Ala Ala	
35 40 45	
Leu Leu Ala Ala Leu Phe Tyr Cys Ala Val Ala Trp Ala Gly Leu Gly	
50 55 60	
Arg Ile Asp Ile Val Ala Ser Ala Ser Arg Lys Ile Val Pro Gly Asp	
65 70 75 80	
Arg Val Lys Leu Val Gln Pro Leu Glu Val Gly Val Val Arg Ala Thr	
85 90 95	
His Val Arg Asp Gly Gln Thr Val Lys Ala Gly Glu Ile Leu Ile Glu	
100 105 110	
Leu Asp Pro Phe Ala Gly Gly Val Asp Val Ala Thr	
115 120	

<210> 5
<211> 747
<212> DNA
<213> Homosapiens

<220>
<223> Artificially generated nucleic acid

<400> 5

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gcgcgtcgccg ccgtgtcgaa tggcacgcag tcgcgtccaca ccaactcgat cgacgaggcg	120
atcgcgctgc cgattgactt ctccggccgg atcgccccca acaccagctg atccagcagc	180
acgagacaga cgtcacggac gcgggtcgaca ctctggcgaa gtcctactac gtggagcgcc	240
tgacggatga cctcgccaag cggggcttggc agctgtatggc agaggtcgag aagatgggtg	300
gcatggcgca ggcgatcgcc accgggttggc cgaagcgccct gatcgagcaa tctgcgacgc	360
aaaagcaggc cgcgatcgat cgcggcgatc aggtgtatcgat gggcgtaaac cgctaccggc	420
ccgaacagga gcaaccgatc gacattattt agatcgacaa ctcgacgggtt cggggctccc	480
agatccggtg tctcgccgaa atcgaaaagg cgcgtgattc aaggaagggtt gagtccgcgc	540
tcggggagct ggcgtgtatt gcccgcacgg gtgagggaaa tctgctggct gcagcgaccg	600

agcccgctcg cgcgccccct accgtcgggg agatgtccga cgccatgcgg caagcattcg 660
 gcgaccacga ggcggtgccg gaggtagtgt cggacgttta cggccgtgcc tatggcacgg 720
 atccgttcat ggatagtcga cgtcggt 747

<210> 6
 <211> 48
 <212> PRT
 <213> Homosapiens

<400> 6
 Asp Pro Cys Asn Asp Ile Val Arg Thr Ala Tyr Glu Ala Leu Ala Ala
 1 5 10 15
 Val Leu Gly Gly Thr Gln Ser Leu His Thr Asn Ser Phe Asp Glu Ala
 20 25 30
 Ile Ala Leu Pro Ile Asp Phe Ser Ala Arg Ile Ala Arg Asn Thr Ser
 35 40 45

<210> 7
 <211> 301
 <212> DNA
 <213> Homosapiens

<220>
 <223> Synthetically generated nucleic acid

<400> 7
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 gccgcgaattc acgctgatcg gacagaatgt caacgcctac cacggcggag ggcccgcacgg 120
 ccgcgtctgg ccgctcggca aattgctgca gcgaactcgcg gacattccag gcgtcatcg 180
 gctgcgttat tcgatcagcc atccgcgcga cgtcgacgac agcctgatcg ccgcgcatcg 240
 cgatttgcggcc ggactgatgc cgttcgtgca cctgcccgtg caatcggggg cggaccggat 300
 c 301

<210> 8
 <211> 91
 <212> PRT
 <213> Homosapiens

<400> 8
 Ile Ile Asp Asp Ile Lys Gln Leu Ala Asp Asn Gly Val Arg Glu Phe
 1 5 10 15
 Thr Leu Ile Gly Gln Asn Val Asn Ala Tyr His Gly Gly Pro Asp
 20 25 30
 Gly Arg Val Trp Pro Leu Gly Lys Leu Leu Gln Arg Leu Ala Asp Ile
 35 40 45
 Pro Gly Val Met Arg Leu Arg Tyr Ser Ile Ser His Pro Arg Asp Val
 50 55 60
 Asp Asp Ser Leu Ile Ala Ala His Arg Asp Leu Pro Gly Leu Met Pro
 65 70 75 80
 Phe Val His Leu Pro Val Gln Ser Gly Ala Asp
 85 90

<210> 9
 <211> 620
 <212> DNA
 <213> Homosapiens

<220>
 <221> misc_feature
 <222> (0)...(0)
 <223> N=A,T,C or G

<400> 9
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ggccttgaac ggacagcgtg cttgagttgg tcggggtcac caccggaccc gtgtccaccg 120
ggcagtcac ngtgaaagca cttgaccatg atcccagacg gtgccgtcat ccgcgcggac 180
ccacancgtt tccgcgcccc accggattga tagctcagcg acaccagctg ggctgccgtg 240
acgtanttgt gctgggttngg tgcaagtgcc acccccgtca agacaaaantg gccgcacctg 300
tgcccggttc ccaaacctca tattgggtcg cagcaactgtc gaacggatca ctgtangtgc 360
acagcgacna anccgcatan ctctngccgt ggggcgcaac gatgttnnac accgtctcaa 420
cgggtaccgt gtcnagggga ncatttacng ggaaagcatt cgaccactcc cccacaccgt 480
gcccgcattt gcgcgcattt ctttcattga tatgtccacg tcggtnnnnc tttaagcngg 540
cggcaaccgc ggtgnagctn cactttttgt tccttttatt ganggttaat ttgcgcgtt 600
tgncgtaan tntttngaan 620

<210> 10

<211> 662

<212> DNA

<213> Homosapiens

<220>

<221> misc_feature

<222> (0)...(0)

<223> N=A,T,C or G

<400> 10
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ctgggtattt cacgcaaccg ctctgcgtt ggcgggaaac accgacgcgc ttgaaggctt 120
accggacgac acgcccggcag cttgattcg aatgcattcg gagtacttgc gcagtcagga 180
ttccgagcag cgcccaagc tgtccgaact ggatcagcaa cgggtgcaga aggtcgcgg 240
gaccaggacg atcgacgcca gcatcgcgaa gattgaagct ttgctgcggg gctgcaggan 300
cgggtcgcccc ttgcgaagta octggcgac agggagtacg gctcaaagct gcaatattcg 360
caggaactcc aggaacttggt cgggatgcag caggacatcc tggtgcaacg gagcaaagct 420
cgagggaaacc aatgcggntt gtcgcgcac ttcgacgaaa acccgcggnna agttcgtct 480
nngaataacc ggcacccgnc tggccnaacg atctggccc aaggggacgc aaaaaaggc 540
cggcaagncc tcaaaggacc aagggnntt taaaancgaa gcacccggga cccaaaccttt 600
aaaaancntt ggcggccccc attcgacggn gtggnggcaaa caaattggc cgngccccat 660
tt 662

<210> 11

<211> 242

<212> DNA

<213> Homosapiens

<220>

<221> misc_feature

<222> (0)...(0)

<223> N=A,T,C or G

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ctatcnctaa agggtctccn acnacgtcca nccggacnag ctgacctcg tttccnnaag 120
cgtgaaactc aaggccgggt aaaccntcnt gttcgctng atcaccatct agtcgcgc 180
cnnngcgcgac aggatcaacg ccaaggtgat ggcgcgttcc cgcctggcgt cgtcgatgg 240
tc 242

<210> 12

<211> 552

<212> DNA

<213> Homosapiens

<400> 12

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ctgttgcstat tcgaacatgt tcacgggtgaa tccccgtgacc gccccaggc gatgggtggac	120
ctgctggcgc agtacgagca gcacgggttg cagtaaaaca gcccgcgaatt accggaccac	180
ctgccgctgt atctggagta cctgtcgcaag ctgccgcaag gcgaagccgt ggaaggttt	240
aaagatatcg cgccgattct ggcattgtcg agcgcgcgtc tgcaacagcg taaaagccgt	300
tatgccgtga tgtttgcatt gctgtgaaa ttggccgata ccgctatcga cagcgacaaa	360
gtggcgaaa aaattgccga cgaagcgcgc gatgatacgc cgcaggcgct ggatgtgtt	420
tggagaagaag agcagggttaa attctttgtc gacaaaggct gcggcgattc agcaatca	480
gctcatcagc gtcgcttgc cggtgccgtc ggcgcgcaat atctgaatat cctcggtgag	540
aggctggaga gt	552

<210> 13
<211> 265
<212> DNA
<213> Homosapiens

<220>
<221> misc_feature
<222> (0)...(0)
<223> N=A,T,C or G

<400> 13	
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ggcggttnaa agtgaacatc cgccgagcac ggcagcgcacg cctccgctca ccgtcngcgc	120
agtacttcct cgggtcgccg cgcctagcac tctgcgcgt gacatcaanc cgtgaaccca	180
cgggagactt tgccgcna agggatgagt ccactattag atgacgcatg gctacgagcc	240
natcctcggt ganaagctgg agagt	265

<210> 14
<211> 317
<212> DNA
<213> Homosapiens

<220>
<221> misc_feature
<222> (0)...(0)
<223> N=A,T,C or G

<400> 14	
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agccgcctg angctctcg cgtaactccg gatgcacggg ggaccgtgac gggtgtantg	120
ccctggcttt tctcagcnga aatctgcaca gccatcttcc gatcgatctg ggcagggtgg	180
ggccgcncaa aacgggtggc atctccaaac cgcaggaacg tttttgcag gatgtcgaac	240
atcatccacg cttcgtncc caacggctac ttcgcccgtt accggccat gtcatcctcg	300
gtganaagct gganant	317

<210> 15
<211> 341
<212> DNA
<213> Homosapiens

<220>
<221> misc_feature
<222> (0)...(0)
<223> N=A,T,C or G

<400> 15	
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ccnccgctgc tctcgatcg cggccagacc tacaccancg acgttagatca agcgcgtgg	120
gcccggcgcn acnagcanca nctaantcaa ggcctcgctg catccgcac atccagcgct	180
cagcttcgca ggaattgcgc gancgcttt ggcgtcncc agtnaccgca tacacacctcg	240

ccgtccctgc gaaagcaagg acccataactc cgcnccgggt gttgttgcg ggactcgta	300
tggcggcaac gcacaacgtn naacttctgt ggttatggat c	341
<210> 16	
<211> 256	
<212> DNA	
<213> Homosapiens	
<220>	
<221> misc_feature	
<222> (0)...(0)	
<223> N=A,T,C or G	
<400> 16	
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ctcggacttc cctgcncaat cnaaggcttc tgcatcncc antacaacta cnacggcaat	120
ctnacatcac gcaagatcgc angctcngtc atcaaggacg cngcggtcnc cnccccggcag	180
gtgctcnata tngtgtgaa naacaccatc gtcctgcaa cggcaagaag atcacatgca	240
aggtccactc gctgtg	256
<210> 17	
<211> 701	
<212> DNA	
<213> Homosapiens	
<220>	
<223> N = A, T, C or G	
<400> 17	
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ctaaacggag gatctcacga acatccgctc caacccgcac accacgctcc cccgcgtcac	120
gacaggctcg ctgcctccct cgcgcaagtt ctggcaatc cctgaggccg ccccccacat	180
ccgcgttccc ttgcgcgaga tcatcctgtc cgagggcgcc ggcgagccga acctgcccgt	240
ctatgacacc tcggggccct acaccgatcc ggcgttgacg atcgacgtca acagcggcct	300
gccgcgcaat cgcctcgccct gggtcaagga acggccggc gtcgaggaat atcangggcg	360
caccatcaag ccggaggaca acggcaatgt cggccatcc cacgcccaca aggcgttcac	420
cgngcaccac aagccgctgc cggnctcga cggcacaaga tcacccactc gagttcgccg	480
cgccggcatt ataccaagga gatgatctac gtcgcccggc gtgagaatct tggncgcaag	540
cagcagctng agcgcgcccga nggccggctn gccgacggna agagtttgg cgccgcggtg	600
ccggncttna ttacccggaa atttgtncgc aangagatcg ncgcgnncgn gccattattt	660
ccttnaaaaa ttaancattg ccgagcttga accgatgaan n	701
<210> 18	
<211> 511	
<212> DNA	
<213> Homosapiens	
<220>	
<223> N=A,T,C or G	
<400> 18	
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aacccgggac gagctggcct tcctgccggc cgccctcgaa attgtcgaga cgccgcacatc	120
tcccaccgcg agactcacgg cccgccttgcg tgctgccttg ttctactgcg ccgtggcgtg	180
ggcgggtctc ggcagatcg acatcggtgc ttctgcatcc agaaagatcg tgccggccga	240
ccgtgtaaag ctggttcagc cgctcgaggt cggcgtggtg cggccactc atgtccgcga	300
tggccaaacc gtcaaggccg gcgagattct gatcgagctg gatccattcg cgggtgggtgt	360
ggatgttgcg ccccgtcnag aggtccatca cgggtgtccgc gccccancgg atcgccacac	420
catcttgcg acctnttctt caccgacgan gtcaccgcgg agttgcccgt attgcgntga	480
tcttancan gaanntgcgg ncgtatgtca t	511

<210> 19
<211> 620
<212> DNA
<213> Homosapiens

<220>
<221> CDS
<222> (1) ... (618)
<223> N= A, T, C or G
Xaa= any amino acid

<223> Synthetically generated nucleic acid

<400> 19
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 Thr Leu Xaa Pro Leu Thr Glu Asp Gln Asn Arg * Arg Ala Lys Thr
 1 5 10 15
 ccg aga acg tct ggc ctt gaa cg^g aca g^c g^c t^t g^t a^g t^g t^c g^g g^g
 Pro Arg Thr Ser Gly Leu Glu Arg Thr Ala Cys Leu Ser Trp Ser Gly
 20 25 30
 tca cca ccg gac ccg t^t c^c a^c c^c g^c c^a g^t t^c aⁿ c^a g^a c^a t^t g^t
 Ser Pro Pro Asp Pro Cys Pro Ala Gln Ser Xaa * Lys His Leu
 35 40 45
 acc atg atc cca gac ggt gcc gtc atc cgc g^c g^c a^c c^c a^a n^t c^t n^t c^t
 Thr Met Ile Pro Asp Gly Ala Val Ile Arg Ala Asp Pro Xaa Arg Xaa
 50 55 60
 cgc gcc cga ccg gat tga tag ctc agc gac acc agc t^g g^c t^c g^c g^t g^t
 Arg Ala Arg Pro Asp * * Leu Ser Asp Thr Ser Trp Ala Ala Val
 65 70 75
 acg tan ttg tgc tgg ttn ggt gca agt gcc acc ccg ctc aag aca aan
 Thr Xaa Leu Cys Trp Xaa Gly Ala Ser Ala Thr Pro Leu Lys Thr Xaa
 80 85 90
 tgg ccg cac ctg tgc ccg t^t c^c a^a a^a c^g t^c a^t t^g g^g t^c c^a c^a
 Trp Pro His Leu Cys Pro Cys Pro Lys Arg His Ile Gly Ser Gln His
 95 100 105
 tgt cga acg gat cac t^t g^t a^{ng} t^c a^c g^c a^c n^a a^a c^c g^a t^c aⁿ c^t
 Cys Arg Thr Asp His Cys Xaa Cys Thr Ala Thr Xaa Pro His Xaa Ser
 110 115 120
 ngc cgt ggg g^c g^c a^a c^g a^t tⁿⁿ a^c a^c c^c t^t c^a c^g g^t a^c c^c t^t
 Xaa Arg Gly Ala Gln Arg Cys Xaa Thr Pro Ser Gln Arg Val Pro Cys
 125 130 135 140
 cna ggg gan cat tta cng gga aag cat tcg acc act ccc cca cac cgt
 Xaa Gly Xaa His Leu Xaa Gly Lys His Ser Thr Thr Pro Pro His Arg
 145 150 155
 gcc cgc att tgc gcc gat tcc ttt cat tga tat gtc cac gtc ggt n^g g
 Ala Arg Ile Cys Ala Asp Ser Phe His * Tyr Val His Val Gly Xaa
 160 165 170
 nct tta agc n^g g^g c^g c^a c^g c^g t^{gn} a^g c^t n^c a^t t^{tt} t^t g^t t^c t^{tt}
 Xaa Leu Ser Xaa Arg Gln Pro Arg Xaa Ser Xaa Thr Phe Cys Ser Phe
 175 180 185

tat tga ngg tta att tgc gcg ctt tgg ncg taa ntn ttt nga
 Tyr * Xaa Leu Ile Cys Ala Leu Trp Xaa * Xaa Phe Xaa
 190 195

618

an 620

<210> 20
 <211> 199
 <212> PRT
 <213> Homosapiens

<220>
 <223> Xaa= any amino acid

<223> Frame shift sequence

<400> 20
 Thr Leu Xaa Pro Leu Thr Glu Asp Gln Asn Arg Arg Ala Lys Thr Pro
 1 5 10 15
 Arg Thr Ser Gly Leu Glu Arg Thr Ala Cys Leu Ser Trp Ser Gly Ser
 20 25 30
 Pro Pro Asp Pro Cys Pro Pro Ala Gln Ser Xaa Lys His Leu Thr Met
 35 40 45
 Ile Pro Asp Gly Ala Val Ile Arg Ala Asp Pro Xaa Arg Xaa Arg Ala
 50 55 60
 Arg Pro Asp Leu Ser Asp Thr Ser Trp Ala Ala Val Thr Xaa Leu Cys
 65 70 75 80
 Trp Xaa Gly Ala Ser Ala Thr Pro Leu Lys Thr Xaa Trp Pro His Leu
 85 90 95
 Cys Pro Cys Pro Lys Arg His Ile Gly Ser Gln His Cys Arg Thr Asp
 100 105 110
 His Cys Xaa Cys Thr Ala Thr Xaa Pro His Xaa Ser Xaa Arg Gly Ala
 115 120 125
 Gln Arg Cys Xaa Thr Pro Ser Gln Arg Val Pro Cys Xaa Gly Xaa His
 130 135 140
 Leu Xaa Gly Lys His Ser Thr Thr Pro Pro His Arg Ala Arg Ile Cys
 145 150 155 160
 Ala Asp Ser Phe His Tyr Val His Val Gly Xaa Xaa Leu Ser Xaa Arg
 165 170 175
 Gln Pro Arg Xaa Ser Xaa Thr Phe Cys Ser Phe Tyr Xaa Leu Ile Cys
 180 185 190
 Ala Leu Trp Xaa Xaa Phe Xaa
 195

<210> 21
 <211> 620
 <212> DNA
 <213> Homosapiens

<220>
 <221> CDS
 <222> (2)...(619)
 <223> N= A, T, C or G
 Xaa= any amino acid

<223> Synthetically generated nucleic acid

<400> 21
 a ctc tcc anc ctc tca ccg agg atc aga ata ggt gaa gag cga aga cac
 Leu Ser Xaa Leu Ser Pro Arg Ile Arg Ile Gly Glu Glu Arg Arg His

49

1	5	10	15	
cga gaa cgt ctg gcc ttg aac gga cag cgt gct tga gtt ggt cgg ggt				97
Arg Glu Arg Leu Ala Leu Asn Gly Gln Arg Ala * Val Gly Arg Gly				
20	25		30	
cac cac cgg acc cgt gtc cac cgg cgc agt cac ngt gaa agc act tga				145
His His Arg Thr Arg Val His Arg Arg Ser His Xaa Glu Ser Thr *				
35	40		45	
cca tga tcc cag acg gtg ccg tca tcc gcg cgg acc cac anc gtn tcc				193
Pro * Ser Gln Thr Val Pro Ser Ser Ala Arg Thr His Xaa Val Ser				
50	55		60	
gcg ccc gac cgg att gat agc tca gcg aca cca gct ggg ctg cgg tga				241
Ala Pro Asp Arg Ile Asp Ser Ser Ala Thr Pro Ala Gly Leu Pro *				
65	70		75	
cgt ant tgt gct ggt tng gtg caa gtg cca ccc cgc tca aga caa ant				289
Arg Xaa Cys Ala Gly Xaa Val Gln Val Pro Pro Arg Ser Arg Gln Xaa				
80	85		90	
ggc cgc acc tgt gcc cgt gtc cca aac gtc ata ttg ggt cgc agc act				337
Gly Arg Thr Cys Ala Arg Val Pro Asn Val Ile Leu Gly Arg Ser Thr				
95	100		105	
gtc gaa cgg atc act gta ngt gca cag cga cna anc cgc ata nct ctn				385
Val Glu Arg Ile Thr Val Xaa Ala Gln Arg Xaa Xaa Arg Ile Xaa Leu				
110	115		120	
gcc gtg ggg cgc aac gat gtt nna cac cgt ctc aac ggg tac cgt gtc				433
Ala Val Gly Arg Asn Asp Val Xaa His Arg Leu Asn Gly Tyr Arg Val				
125	130		135	140
nag ggg anc att tac ngg gaa agc att cga cca ctc ccc cac acc gtg				481
Xaa Gly Xaa Ile Tyr Xaa Glu Ser Ile Arg Pro Leu Pro His Thr Val				
145	150		155	
ccc gca ttt gcg ccg att cct ttc att gat atg tcc acg tcg gtn ggn				529
Pro Ala Phe Ala Pro Ile Pro Phe Ile Asp Met Ser Thr Ser Val Gly				
160	165		170	
ctt taa gcn ggc ggc aac cgc ggt gna gct nca ctt ttt gtt cct ttt				577
Leu * Ala Gly Gly Asn Arg Gly Xaa Ala Xaa Leu Phe Val Pro Phe				
175	180		185	
att gan ggt taa ttt gcg cgc ttt ggn cgt aan tnt ttn gaa				619
Ile Xaa Gly * Phe Ala Arg Phe Gly Arg Xaa Xaa Xaa Glu				
190	195		200	
n				620

<210> 22
<211> 200
<212> PRT
<213> Homosapiens

<220>
<223> Xaa= any amino acid
<223> Frame shift sequence

BI
 Cont'd

<400> 22
 Leu Ser Xaa Leu Ser Pro Arg Ile Arg Ile Gly Glu Glu Arg Arg His
 1 5 10 15
 Arg Glu Arg Leu Ala Leu Asn Gly Gln Arg Ala Val Gly Arg Gly His
 20 25 30
 His Arg Thr Arg Val His Arg Arg Ser His Xaa Glu Ser Thr Pro Ser
 35 40 45
 Gln Thr Val Pro Ser Ser Ala Arg Thr His Xaa Val Ser Ala Pro Asp
 50 55 60
 Arg Ile Asp Ser Ser Ala Thr Pro Ala Gly Leu Pro Arg Xaa Cys Ala
 65 70 75 80
 Gly Xaa Val Gln Val Pro Pro Arg Ser Arg Gln Xaa Gly Arg Thr Cys
 85 90 95
 Ala Arg Val Pro Asn Val Ile Leu Gly Arg Ser Thr Val Glu Arg Ile
 100 105 110
 Thr Val Xaa Ala Gln Arg Xaa Xaa Arg Ile Xaa Leu Ala Val Gly Arg
 115 120 125
 Asn Asp Val Xaa His Arg Leu Asn Gly Tyr Arg Val Xaa Gly Xaa Ile
 130 135 140
 Tyr Xaa Glu Ser Ile Arg Pro Leu Pro His Thr Val Pro Ala Phe Ala
 145 150 155 160
 Pro Ile Pro Phe Ile Asp Met Ser Thr Ser Val Gly Leu Ala Gly Gly
 165 170 175
 Asn Arg Gly Xaa Ala Xaa Leu Phe Val Pro Phe Ile Xaa Gly Phe Ala
 180 185 190
 Arg Phe Gly Arg Xaa Xaa Xaa Glu
 195 200

<210> 23

<211> 620

<212> DNA

<213> Homosapiens

<220>

<221> CDS

<222> (3) ... (620)

<223> N= A, T, C or G
Xaa= any amino acid

<223> Synthetically generated nucleic acid

<400> 23
 ac tct cca ncc tct cac cga gga tca gaa tag gtg aag agc gaa gac 47
 Ser Pro Xaa Ser His Arg Gly Ser Glu * Val Lys Ser Glu Asp
 1 5 10

acc gag aac gtc tgg cct tga acg gac agc gtg ctt gag ttg gtc ggg 95
 Thr Glu Asn Val Trp Pro * Thr Asp Ser Val Leu Glu Leu Val Gly
 15 20 25

gtc acc acc gga ccc gtg tcc acc ggc gca gtc acn gtg aaa gca ctt 143
 Val Thr Thr Gly Pro Val Ser Thr Gly Ala Val Thr Val Lys Ala Leu

30 35 40 45

gac cat gat ccc aga cgg tgc cgt cat ccg cgc gga ccc aca ncg tnt 191
 Asp His Asp Pro Arg Arg Cys Arg His Pro Arg Gly Pro Thr Xaa Xaa

50 55 60

ccg cgc ccg acc gga ttg ata gct cag cga cac cag ctg ggc tgc cgt 239
 Pro Arg Pro Thr Gly Leu Ile Ala Gln Arg His Gln Leu Gly Cys Arg

65

70

75

gac gta ntt gtg ctg gtt ngg tgc aag tgc cac ccc gct caa gac aaa Asp Val Xaa Val Leu Val Xaa Cys Lys Cys His Pro Ala Gln Asp Lys	287
80 85 90	
ntg gcc gca cct gtg ccc gtg tcc caa acg tca tat tgg gtc gca gca Xaa Ala Ala Pro Val Pro Val Ser Gln Thr Ser Tyr Trp Val Ala Ala	335
95 100 105	
ctg tcg aac gga tca ctg tan gtg cac agc gac naa ncc gca tan ctc Leu Ser Asn Gly Ser Leu Xaa Val His Ser Asp Xaa Xaa Ala Xaa Leu	383
110 115 120 125	
tng ccg tgg ggc gca acg atg ttn nac acc gtc tca acg ggt acc gtc Xaa Pro Trp Gly Ala Thr Met Xaa Xaa Thr Val Ser Thr Gly Thr Val	431
130 135 140	
tcn agg gga nca ttt acn ggg aaa gca ttc gac cac tcc ccc aca ccg Ser Arg Gly Xaa Phe Thr Gly Lys Ala Phe Asp His Ser Pro Thr Pro	479
145 150 155	
tgc ccg cat ttg cgc cga ttc ctt tca ttg ata tgt cca cgt cggt tng Cys Pro His Leu Arg Arg Phe Leu Ser Leu Ile Cys Pro Arg Arg Xaa	527
160 165 170	
gnc ttt aag cng gcg gca acc gcg gtg nag ctn cac ttt ttg ttc ctt Xaa Phe Lys Xaa Ala Ala Thr Ala Val Xaa Leu His Phe Leu Phe Leu	575
175 180 185	
tta ttg ang gtt aat ttg cgc gct ttg gnc gta ant ntt tng aan Leu Leu Xaa Val Asn Leu Arg Ala Leu Xaa Val Xaa Xaa Xaa	620
190 195 200	

<210> 24

<211> 204

<212> PRT

<213> Homosapiens

<220>

<223> Xaa= any amino acid

<223> Frame shift sequence

<400> 24

Ser Pro Xaa Ser His Arg Gly Ser Glu Val Lys Ser Glu Asp Thr Glu
 1 5 10 15
 Asn Val Trp Pro Thr Asp Ser Val Leu Glu Leu Val Gly Val Thr Thr
 20 25 30
 Gly Pro Val Ser Thr Gly Ala Val Thr Val Lys Ala Leu Asp His Asp
 35 40 45
 Pro Arg Arg Cys Arg His Pro Arg Gly Pro Thr Xaa Xaa Pro Arg Pro
 50 55 60
 Thr Gly Leu Ile Ala Gln Arg His Gln Leu Gly Cys Arg Asp Val Xaa
 65 70 75 80
 Val Leu Val Xaa Cys Lys Cys His Pro Ala Gln Asp Lys Xaa Ala Ala
 85 90 95
 Pro Val Pro Val Ser Gln Thr Ser Tyr Trp Val Ala Ala Leu Ser Asn
 100 105 110
 Gly Ser Leu Xaa Val His Ser Asp Xaa Xaa Ala Xaa Leu Xaa Pro Trp

115	120	125
Gly Ala Thr Met Xaa Xaa Thr Val Ser Thr Gly		Thr Val Ser Arg Gly
130	135	140
Xaa Phe Thr Gly Lys Ala Phe Asp His Ser Pro		Thr Pro Cys Pro His
145	150	155
Leu Arg Arg Phe Leu Ser Leu Ile Cys Pro Arg Arg		Xaa Xaa Phe Lys
165	170	175
Xaa Ala Ala Thr Ala Val Xaa Leu His Phe Leu Phe Leu Leu Xaa		
180	185	190
Val Asn Leu Arg Ala Leu Xaa Val Xaa Xaa Xaa		
195	200	

<210> 25

<211> 619

<212> DNA

<213> Homosapiens

<220>

<223> N= A,T,C or G

<223> Synthetically generated nucleic acid

<223> Reverse strand

<400> 25	60
nttcnaana nttacgncca aagcgcgcaa attaacccntc aataaaaagga acaaaaagtg	120
nagctncacc gcgggtgccg cncgcttaaa gnccnaccga cgtggacata tcaatgaaag	180
gaatcgccgc aaatgcgggc acgggtgtggg ggagggtgtcg aatgcttcc cngtaatgn	240
tccccctngac acggtaacccg ttgagacggt gtnnaacatc gttgcgc(ccc acggcnagag	300
ntatcggnnt tngtcgtgt gcacntacag tgatccgttc gacagtgtcg cgacccaata	360
tgacgtttgg gacacgggca caggtgcggc canttgcgt tgagcgggtg gcacttgac	420
cnaaccagca caantacgtc acggcagccc agctgggtgc gctgagctat caatccggtc	480
gggcgcggan acgntgtggg tccgcgcgga tgacggcacc gtctgggatc atggtaagt	540
gtttcacng tgactgcgcc ggtggacacg ggtccgggtgg tgaccccgac caactcaagc	600
acgctgtccg ttcaaggcca gacgttctcg gtgtcttcgc tcttcaccta ttctgatcct	619
cggtgagagg ntggagagt	

<210> 26

<211> 200

<212> PRT

<213> Homosapiens

<220>

<223> Xaa= any amino acid

<223> Frame shift sequence

<223> Reverse strand

<400> 26	15
Xaa Xaa Xaa Xaa Tyr Xaa Gln Ser Ala Gln Ile Asn Xaa Gln Lys Glu	
1 5 10 15	
Gln Lys Val Xaa Xaa His Arg Gly Cys Arg Xaa Leu Lys Xaa Xaa Pro	
20 25 30	
Thr Trp Thr Tyr Gln Lys Glu Ser Ala Gln Met Arg Ala Arg Cys Gly	
35 40 45	
Gly Val Val Glu Cys Phe Pro Xaa Lys Xaa Ser Pro Xaa His Gly Thr	
50 55 60	
Arg Asp Gly Xaa Xaa His Arg Cys Ala Pro Arg Xaa Glu Xaa Cys Xaa	
65 70 75 80	
Xaa Val Ala Val His Xaa Gln Ser Val Arg Gln Cys Cys Asp Pro Ile	

85	90	95
Arg Leu Gly His Gly His Arg Cys Gly Xaa Phe Val Leu Ser Gly Val		
100	105	110
Ala Leu Ala Xaa Asn Gln His Xaa Tyr Val Arg Ala Ala Gln Leu Val		
115	120	125
Ser Leu Ser Tyr Gln Ser Gly Arg Ala Arg Xaa Xaa Cys Gly Ser Ala		
130	135	140
Arg Met Thr Ala Pro Ser Gly Ile Met Val Lys Cys Phe His Xaa Asp		
145	150	155
Cys Ala Gly Gly His Gly Ser Gly Gly Asp Pro Asp Gln Leu Lys His		
165	170	175
Ala Val Arg Ser Arg Pro Asp Val Leu Gly Val Phe Ala Leu His Leu		
180	185	190
Phe Ser Ser Val Arg Xaa Trp Arg		
195	200	

<210> 27

<211> 202

<212> PRT

<213> Homosapiens

<220>

<223> Xaa= any amino acid

<223> Frame shift sequence

<223> Reverse strand

<400> 27

Phe Xaa Xaa Xaa Thr Xaa Lys Ala Arg Lys Leu Thr Xaa Asn Lys Arg			
1	5	10	15
Asn Lys Lys Xaa Ser Xaa Thr Ala Val Ala Ala Xaa Leu Lys Xaa Xaa			
20	25	30	
Arg Arg Gly His Ile Asn Glu Arg Asn Arg Arg Lys Cys Gly His Gly			
35	40	45	
Val Gly Glu Trp Ser Asn Ala Phe Xaa Val Asn Xaa Pro Xaa Asp Thr			
50	55	60	
Val Pro Val Glu Thr Val Xaa Asn Ile Val Ala Pro His Gly Xaa Xaa			
65	70	75	80
Tyr Ala Xaa Xaa Ser Leu Cys Xaa Tyr Ser Asp Pro Phe Asp Ser Ala			
85	90	95	
Ala Thr Gln Tyr Asp Val Trp Asp Thr Gly Thr Gly Ala Ala Xaa Leu			
100	105	110	
Ser Ala Gly Trp His Leu His Xaa Thr Ser Thr Xaa Thr Ser Arg Gln			
115	120	125	
Pro Ser Trp Cys Arg Ala Ile Asn Pro Val Gly Arg Gly Xaa Xaa Val			
130	135	140	
Gly Pro Arg Gly Arg His Arg Leu Gly Ser Trp Ser Ser Ala Phe Xaa			
145	150	155	160
Val Thr Ala Pro Val Asp Thr Gly Pro Val Val Thr Pro Thr Asn Ser			
165	170	175	
Ser Thr Leu Ser Val Gln Gly Gln Thr Phe Ser Val Ser Ser Leu Phe			
180	185	190	
Thr Tyr Ser Asp Pro Arg Glu Xaa Gly Glu			
195	200		

<210> 28

<211> 201

<212> PRT

<213> Homosapiens

<220>

<223> Xaa= any amino acid

<223> Frame shift sequence

<223> Reverse strand

<400> 28

Xaa	Lys	Xaa	Leu	Xaa	Pro	Lys	Arg	Ala	Asn	Xaa	Ser	Ile	Lys	Gly	Thr
1					5				10				15		
Lys	Ser	Xaa	Ala	Xaa	Pro	Arg	Leu	Pro	Xaa	Ala	Xaa	Thr	Asp	Val	
					20				25			30			
Asp	Ile	Ser	Met	Lys	Gly	Ile	Gly	Ala	Asn	Ala	Gly	Thr	Val	Trp	Gly
					35				40			45			
Ser	Gly	Arg	Met	Leu	Ser	Xaa	Met	Xaa	Pro	Xaa	Thr	Arg	Tyr	Pro	Leu
					50				55			60			
Arg	Arg	Cys	Xaa	Thr	Ser	Leu	Arg	Pro	Thr	Xaa	Arg	Xaa	Met	Arg	Xaa
					65				70			75			80
Xaa	Arg	Cys	Ala	Xaa	Thr	Val	Ile	Arg	Ser	Thr	Val	Leu	Arg	Pro	Asn
					85				90			95			
Met	Thr	Phe	Gly	Thr	Arg	Ala	Gln	Val	Arg	Pro	Xaa	Cys	Leu	Glu	Arg
					100				105			110			
Gly	Gly	Thr	Cys	Thr	Xaa	Pro	Ala	Gln	Xaa	Arg	His	Gly	Ser	Pro	Ala
					115				120			125			
Gly	Val	Ala	Glu	Leu	Ser	Ile	Arg	Ser	Gly	Ala	Xaa	Thr	Xaa	Trp	Val
					130				135			140			
Arg	Ala	Asp	Asp	Gly	Thr	Val	Trp	Asp	His	Gly	Gln	Val	Leu	Ser	Xaa
					145				150			155			160
Leu	Arg	Arg	Trp	Thr	Arg	Val	Arg	Trp	Pro	Arg	Pro	Thr	Gln	Ala	Arg
					165				170			175			
Cys	Pro	Phe	Lys	Ala	Arg	Arg	Ser	Arg	Cys	Leu	Arg	Ser	Ser	Pro	Ile
					180				185			190			
Leu	Ile	Leu	Gly	Glu	Arg	Xaa	Glu	Ser							
					195				200						

<210> 29

<211> 662

<212> DNA

<213> Homosapiens

<220>

<221> CDS

<222> (1)...(660)

<223> N= A,T,C or G

Xaa= any amino acid

<223> Synthetically generated nucleic acid

<400> 29

gat	ccg	acc	agc	aat	cag	gcg	gag	ctg	cag	cac	ctg	aaa	aac	gac	ctt
1									5			10			15
Asp	Pro	Thr	Ser	Asn	Gln	Ala	Glu	Leu	Gln	His	Leu	Lys	Asn	Asp	Leu

ctc	tcg	gca	ctg	ctg	ggt	att	tca	cgc	aac	cgc	tct	gcg	ctt	ggc	ggg
Leu	Ser	Ala	Leu	Leu	Gly	Ile	Ser	Arg	Asn	Arg	Ser	Ala	Leu	Gly	Gly
					20				25			30			

aaa	cac	cga	cgc	gct	tga	agg	ctt	acc	gga	cga	cac	gcc	gcc	agc	ctt
Lys	His	Arg	Arg	Ala	*	Arg	Leu	Thr	Gly	Arg	His	Ala	Ala	Ser	Leu
					35				40			45			

48

96

144

gat tcg aat gca tct gga gta ctt gcg cag tca gga ttc cga gca gcg Asp Ser Asn Ala Ser Gly Val Leu Ala Gln Ser Gly Phe Arg Ala Ala	192
50 55 60	
cgc caa gct gtc cga act gga tca gca acg ggt gca gaa ggt cgc gga Arg Gln Ala Val Arg Thr Gly Ser Ala Thr Gly Ala Glu Gly Arg Gly	240
65 70 75	
gac cag gac gat cga cgc cag cat cgc gaa gat tga agc ttt gct gcg Asp Gln Asp Asp Arg Arg Gln His Arg Glu Asp * Ser Phe Ala Ala	288
80 85 90	
gtg ctg cag gan cgg gtc ggg gtt cgc aag tac ctg gcg gac agg gag Val Leu Gln Xaa Arg Val Gly Val Arg Lys Tyr Leu Ala Asp Arg Glu	336
95 100 105 110	
tac ggc tca aag ctg caa tat tcg cag gaa ctc cag gaa ctg gtc ggg Tyr Gly Ser Lys Leu Gln Tyr Ser Gln Glu Leu Gln Glu Leu Val Gly	384
115 120 125	
atg cag cag gac atc ctg gtg caa cgg agc aaa gct cga gga aac caa Met Gln Gln Asp Ile Leu Val Gln Arg Ser Lys Ala Arg Gly Asn Gln	432
130 135 140	
tgc ggn ttg tcg ccg cac ttc gac gaa aac ccg cgg naa gct tcg tct Cys Gly Leu Ser Pro His Phe Asp Glu Asn Pro Arg Xaa Ala Ser Ser	480
145 150 155	
nng aat aac cgg cac ccg nct gtt ccn acg atc ttg gcc caa ggg gac Xaa Asn Asn Arg His Pro Xaa Val Pro Thr Ile Leu Ala Gln Gly Asp	528
160 165 170	
gca aaa aag ggc cgg caa gnc ctc aaa gga cca agg gng ttt taa aan Ala Lys Lys Gly Arg Gln Xaa Leu Lys Gly Pro Arg Xaa Phe * Xaa	576
175 180 185	
ccg agc acc cgg gac cca acc ttt aaa aan cnt tgg cgg ccc cca ttc Pro Ser Thr Arg Asp Pro Thr Phe Lys Xaa Xaa Trp Arg Pro Pro Phe	624
190 195 200 205	
gac ggn gtg gng gca aca aat tgg gcc gng ccc cat tt Asp Gly Val Xaa Ala Thr Asn Trp Ala Xaa Pro His	662
210 215	

<210> 30
<211> 217
<212> PRT
<213> Homosapiens

<220>
<223> Xaa= any amino acid

<223> Frame shift sequence

<400> 30
Asp Pro Thr Ser Asn Gln Ala Glu Leu Gln His Leu Lys Asn Asp Leu
1 5 10 15
Leu Ser Ala Leu Leu Gly Ile Ser Arg Asn Arg Ser Ala Leu Gly Gly
20 25 30
Lys His Arg Arg Ala Arg Leu Thr Gly Arg His Ala Ala Ser Leu Asp

35	40	45
Ser Asn Ala Ser Gly Val Leu Ala Gln Ser Gly Phe Arg Ala Ala Arg		
50	55	60
Gln Ala Val Arg Thr Gly Ser Ala Thr Gly Ala Glu Gly Arg Gly Asp		
65	70	75
Gln Asp Asp Arg Arg Gln His Arg Glu Asp Ser Phe Ala Ala Val Leu		80
85	90	95
Gln Xaa Arg Val Gly Val Arg Lys Tyr Leu Ala Asp Arg Glu Tyr Gly		
100	105	110
Ser Lys Leu Gln Tyr Ser Gln Glu Leu Gln Glu Leu Val Gly Met Gln		
115	120	125
Gln Asp Ile Leu Val Gln Arg Ser Lys Ala Arg Gly Asn Gln Cys Gly		
130	135	140
Leu Ser Pro His Phe Asp Glu Asn Pro Arg Xaa Ala Ser Ser Xaa Asn		
145	150	155
Asn Arg His Pro Xaa Val Pro Thr Ile Leu Ala Gln Gly Asp Ala Lys		160
165	170	175
Lys Gly Arg Gln Xaa Leu Lys Gly Pro Arg Xaa Phe Xaa Pro Ser Thr		
180	185	190
Arg Asp Pro Thr Phe Lys Xaa Xaa Trp Arg Pro Pro Phe Asp Gly Val		
195	200	205
Xaa Ala Thr Asn Trp Ala Xaa Pro His		
210	215	

<210> 31

<211> 662

<212> DNA

<213> Homosapiens

<220>

<221> CDS

<222> (2)...(661)

<223> N= A,T,C or G

Xaa= any amino acid

<223> Synthetically generated nucleic acid

<400> 31

g atc cga cca gca atc agg cgg agc tgc agc acc tga aaa acg acc ttc	49	
Ile Arg Pro Ala Ile Arg Arg Ser Cys Ser Thr * Lys Thr Thr Phe		
1	5	10
		15

tct cgg cac tgc tgg gta ttt cac gca acc gct ctg cgc ttg gcg gga	97	
Ser Arg His Cys Trp Val Phe His Ala Thr Ala Leu Arg Leu Ala Gly		
20	25	30

aac acc gac gcg ctt gaa ggc tta ccg gac gac acg ccg cca gcc ttg	145	
Asn Thr Asp Ala Leu Glu Gly Leu Pro Asp Asp Thr Pro Pro Ala Leu		
35	40	45

att cga atg cat ctg gag tac ttg cgc agt cag gat tcc gag cag cgc	193	
Ile Arg Met His Leu Glu Tyr Leu Arg Ser Gln Asp Ser Glu Gln Arg		
50	55	60

gcc aag ctg tcc gaa ctg gat cag caa cgg gtg cag aag gtc gcg gag	241	
Ala Lys Leu Ser Glu Leu Asp Gln Gln Arg Val Gln Lys Val Ala Glu		
65	70	75

acc agg acg atc gac gcc agc atc gcg aag att gaa gct ttg ctg cgg	289	
Thr Arg Thr Ile Asp Ala Ser Ile Ala Lys Ile Glu Ala Leu Leu Arg		
80	85	90
		95

tgc tgc agg anc ggg tcg ggg ttc gca agt acc tgg cgg aca ggg agt Cys Cys Arg Xaa Gly Ser Gly Phe Ala Ser Thr Trp Arg Thr Gly Ser 100 105 110	337
acg gct caa agc tgc aat att cgc agg aac tcc agg aac tgg tcg gga Thr Ala Gln Ser Cys Asn Ile Arg Arg Asn Ser Arg Asn Trp Ser Gly 115 120 125	385
tgc agc agg aca tcc tgg tgc aac gga gca aag ctc gag gaa acc aat Cys Ser Arg Thr Ser Trp Cys Asn Gly Ala Lys Leu Glu Glu Thr Asn 130 135 140	433
gcg gnt tgt cgc cgc act tcg acg aaa acc cgc ggn aag ctt cgt ctn Ala Xaa Cys Arg Arg Thr Ser Thr Lys Thr Arg Gly Lys Leu Arg Leu 145 150 155	481
nga ata acc ggc acc cgn ctg ttc cna cga tct tgg ccc aag ggg acg Xaa Ile Thr Gly Thr Arg Leu Phe Xaa Arg Ser Trp Pro Lys Gly Thr 160 165 170 175	529
caa aaa agg gcc ggc aag ncc tca aag gac caa ggg ngt ttt aaa anc Gln Lys Arg Ala Gly Lys Xaa Ser Lys Asp Gln Gly Xaa Phe Lys Xaa 180 185 190	577
cga gca ccc ggg acc caa cct tta aaa anc ntt ggc ggc ccc cat tcg Arg Ala Pro Gly Thr Gln Pro Leu Lys Xaa Xaa Gly Gly Pro His Ser 195 200 205	625
acg gng tgg ngg caa caa att ggg ccg ngc ccc att t Thr Xaa Trp Xaa Gln Gln Ile Gly Pro Xaa Pro Ile 210 215	662

<210> 32
<211> 219
<212> PRT
<213> Homosapiens

<220>
<223> Xaa= any amino acid

<223> Frame shift sequence

<400> 32
Ile Arg Pro Ala Ile Arg Arg Ser Cys Ser Thr Lys Thr Thr Phe Ser
1 5 10 15
Arg His Cys Trp Val Phe His Ala Thr Ala Leu Arg Leu Ala Gly Asn
20 25 30
Thr Asp Ala Leu Glu Gly Leu Pro Asp Asp Thr Pro Pro Ala Leu Ile
35 40 45
Arg Met His Leu Glu Tyr Leu Arg Ser Gln Asp Ser Glu Gln Arg Ala
50 55 60
Lys Leu Ser Glu Leu Asp Gln Gln Arg Val Gln Lys Val Ala Glu Thr
65 70 75 80
Arg Thr Ile Asp Ala Ser Ile Ala Lys Ile Glu Ala Leu Leu Arg Cys
85 90 95
Cys Arg Xaa Gly Ser Gly Phe Ala Ser Thr Trp Arg Thr Gly Ser Thr
100 105 110
Ala Gln Ser Cys Asn Ile Arg Arg Asn Ser Arg Asn Trp Ser Gly Cys
115 120 125

Ser Arg Thr Ser Trp Cys Asn Gly Ala Lys Leu Glu Glu Thr Asn Ala
 130 135 140
 Xaa Cys Arg Arg Thr Ser Thr Lys Thr Arg Gly Lys Leu Arg Leu Xaa
 145 150 155 160
 Ile Thr Gly Thr Arg Leu Phe Xaa Arg Ser Trp Pro Lys Gly Thr Gln
 165 170 175
 Lys Arg Ala Gly Lys Xaa Ser Lys Asp Gln Gly Xaa Phe Lys Xaa Arg
 180 185 190
 Ala Pro Gly Thr Gln Pro Leu Lys Xaa Xaa Gly Gly Pro His Ser Thr
 195 200 205
 Xaa Trp Xaa Gln Gln Ile Gly Pro Xaa Pro Ile
 210 215

<210> 33

<211> 662

<212> DNA

<213> Homosapiens

<220>

<221> CDS

<222> (3)...(662)

<223> N= A,T,C or G

Xaa= any amino acid

<223> Synthetically generated nucleic acid

<400> 33

ga tcc gac cag caa tca ggc gga gct gca gca cct gaa aaa cga cct	47
Ser Asp Gln Gln Ser Gly Gly Ala Ala Ala Pro Glu Lys Arg Pro	
1 5 10 15	

tct ctc ggc act gct ggg tat ttc acg caa ccg ctc tgc gct tgg cgg	95
Ser Leu Gly Thr Ala Gly Tyr Phe Thr Gln Pro Leu Cys Ala Trp Arg	
20 25 30	

gaa aca ccg acg cgc ttg aag gct tac ccg acg aca cgc cgc cag cct	143
Glu Thr Pro Thr Arg Leu Lys Ala Tyr Arg Thr Thr Arg Arg Gln Pro	
35 40 45	

tga ttc gaa tgc atc tgg agt act tgc gca gtc agg att ccg agc agc	191
* Phe Glu Cys Ile Trp Ser Thr Cys Ala Val Arg Ile Pro Ser Ser	
50 55 60	

gcg cca agc tgt ccg aac tgg atc agc aac ggg tgc aga agg tcg cgg	239
Ala Pro Ser Cys Pro Asn Trp Ile Ser Asn Gly Cys Arg Arg Ser Arg	
65 70 75	

aga cca gga cga tcg acg cca gca tcg cga aga ttg aag ctt tgc tgc	287
Arg Pro Gly Arg Ser Thr Pro Ala Ser Arg Arg Leu Lys Leu Cys Cys	
80 85 90	

ggt gct gca gga ncg ggt cgg ggt tcg caa gta cct ggc gga cag gga	335
Gly Ala Ala Gly Xaa Gly Arg Gly Ser Gln Val Pro Gly Gly Gln Gly	
95 100 105 110	

gta cgg ctc aaa gct gca ata ttc gca gga act cca gga act ggt cgg	383
Val Arg Leu Lys Ala Ala Ile Phe Ala Gly Thr Pro Gly Thr Gly Arg	
115 120 125	

gat gca gca gga cat cct ggt gca acg gag caa agc tcg agg aaa cca	431
Asp Ala Ala Gly His Pro Gly Ala Thr Glu Gln Ser Ser Arg Lys Pro	

130

135

140

<210> 34
<211> 217
<212> PRT
<213> Homosapiens

<220>
<223> Xaa= any amino acid
<223> Frame shift sequenc

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<400> 34
Ser Asp Gln Gln Ser Gly Gly Ala Ala Ala Pro Glu Lys Arg Pro Ser
      5          10          15
1
Leu Gly Thr Ala Gly Tyr Phe Thr Gln Pro Leu Cys Ala Trp Arg Glu
      20          25          30
Thr Pro Thr Arg Leu Lys Ala Tyr Arg Thr Thr Arg Arg Gln Pro Phe
      35          40          45
Glu Cys Ile Trp Ser Thr Cys Ala Val Arg Ile Pro Ser Ser Ala Pro
      50          55          60
Ser Cys Pro Asn Trp Ile Ser Asn Gly Cys Arg Arg Ser Arg Arg Pro
65
      70          75          80
Gly Arg Ser Thr Pro Ala Ser Arg Arg Leu Lys Leu Cys Cys Gly Ala
      85          90          95
Ala Gly Xaa Gly Arg Gly Ser Gln Val Pro Gly Gly Gln Gly Val Arg
      100         105         110
Leu Lys Ala Ala Ile Phe Ala Gly Thr Pro Gly Thr Gly Arg Asp Ala
      115         120         125
Ala Gly His Pro Gly Ala Thr Glu Gln Ser Ser Arg Lys Pro Met Arg
      130         135         140
Xaa Val Ala Ala Leu Arg Arg Lys Pro Ala Xaa Ser Phe Val Xaa Glu
      145         150         155         160
Pro Ala Pro Xaa Cys Ser Xaa Asp Leu Gly Pro Arg Gly Arg Lys Lys
      165         170         175
Gly Pro Ala Xaa Pro Gln Arg Thr Lys Gly Val Leu Lys Xaa Glu His
      180         185         190
Pro Gly Pro Asn Leu Lys Xaa Leu Ala Ala Pro Ile Arg Arg Xaa Gly
      195         200         205
Gly Asn Lys Leu Gly Arg Ala Pro Phe

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210

215

<210> 35
<211> 661
<212> DNA
<213> Homosapiens

<220>
<223> N= A, T, C or G

<223> Frame shift sequence

<223> Reverse strand

<400> 35
aaatggggcn cggcccaatt ttttgcnncc acnccgtcga atggggggcg ccaangnttt 60
ttaaagggtt ggtccgggt gctcggnntt taaaacnccc ttgggtccccc gaggncctgc 120
cggccctttt ttgcgtcccc ttgggccaag atcgtnngaa cagnccgggtg ccgttattc 180
nnagacgaag cttncgcgg gtttcgtcg aagtgcggcg acaanccca ttggttccct 240
cgagcttgc tccgttgcac caggatgtcc tgctgcattcc cgaccaggcc ctggagttcc 300
tgcaaatatt gcagcttga gccgtactcc ctgtccgcca ggtacttgcg aaccgcaccc 360
gntcctgcag caccgcagca aagcttcaat cttcgcgatg ctggcgtcga tcgtcctgg 420
ctccgcgacc ttctgcaccc gttgctgatc cagttcggac agcttggcg gctgctcgga 480
atcctgactg cgcaagtact ccagatgtcat tcgaatcaag gctggcgccg tgtcgtccgg 540
taaggcttca agcgcgtcgg ttttccgc caagcgcaga gcgggttgcgt gaaataccca 600
gcagtgccga gagaaggctg ttttcaggt gctgcagctc cgccctgattt ctggcgtggat 660
c 661

<210> 36

<211> 218

<212> PRT

<213> Homosapiens

<220>

<223> Xaa= any amino acid

<223> Frame shift sequence

<223> Reverse strand

<400> 36
Lys Trp Gly Xaa Ala Gln Phe Val Ala Xaa Xaa Pro Ser Asn Gly Gly
1 5 10 15
Arg Gln Xaa Phe Leu Lys Val Gly Ser Arg Val Leu Xaa Phe Asn Xaa
20 25 30
Leu Gly Pro Leu Arg Xaa Cys Arg Pro Phe Phe Ala Ser Pro Trp Ala
35 40 45
Lys Ile Xaa Gly Thr Xaa Gly Cys Arg Leu Phe Xaa Asp Glu Ala Xaa
50 55 60
Arg Gly Phe Ser Ser Lys Cys Gly Asp Xaa Pro His Trp Phe Pro Arg
65 70 75 80
Ala Leu Leu Arg Cys Thr Arg Met Ser Cys Cys Ile Pro Thr Ser Ser
85 90 95
Trp Ser Ser Cys Glu Tyr Cys Ser Phe Glu Pro Tyr Ser Leu Ser Ala
100 105 110
Arg Tyr Leu Arg Thr Pro Thr Xaa Ser Cys Ser Thr Ala Ala Lys Leu
115 120 125
Gln Ser Ser Arg Cys Trp Arg Arg Ser Ser Trp Ser Pro Arg Pro Ser
130 135 140
Ala Pro Val Ala Asp Pro Val Arg Thr Ala Trp Arg Ala Ala Arg Asn
145 150 155 160

Pro Asp Cys Ala Ser Thr Pro Asp Ala Phe Glu Ser Arg Leu Ala Ala
 165 170 175
 Cys Arg Pro Val Ser Leu Gln Ala Arg Arg Cys Phe Pro Pro Ser Ala
 180 185 190
 Glu Arg Leu Arg Glu Ile Pro Ser Ser Ala Glu Arg Arg Ser Phe Phe
 195 200 205
 Arg Cys Cys Ser Ser Ala Leu Leu Val Gly
 210 215

<210> 37

<211> 217

<212> PRT

<213> Homosapiens

<220>

<223> Xaa= any amino acid

<223> Frame shift sequence

<223> Reverse strand

<400> 37

Asn Gly Xaa Arg Pro Asn Leu Leu Xaa Pro Xaa Arg Arg Met Gly Ala
 1 5 10 15
 Ala Xaa Xaa Phe Arg Leu Gly Pro Gly Cys Ser Xaa Phe Lys Xaa Pro
 20 25 30
 Leu Val Leu Xaa Leu Ala Gly Pro Phe Leu Arg Pro Leu Gly Pro Arg
 35 40 45
 Ser Xaa Glu Gln Xaa Gly Ala Gly Tyr Xaa Xaa Thr Lys Leu Xaa Ala
 50 55 60
 Gly Phe Arg Arg Ser Ala Ala Thr Xaa Arg Ile Gly Phe Leu Glu Leu
 65 70 75 80
 Cys Ser Val Ala Pro Gly Cys Pro Ala Ala Ser Arg Pro Val Pro Gly
 85 90 95
 Val Pro Ala Asn Ile Ala Ala Leu Ser Arg Thr Pro Cys Pro Pro Gly
 100 105 110
 Thr Cys Glu Pro Arg Pro Xaa Pro Ala Ala Pro Gln Gln Ser Phe Asn
 115 120 125
 Leu Arg Asp Ala Gly Val Asp Arg Pro Gly Leu Arg Asp Leu Leu His
 130 135 140
 Pro Leu Leu Ile Gln Phe Gly Gln Leu Gly Ala Leu Leu Gly Ile Leu
 145 150 155 160
 Thr Ala Gln Val Leu Gln Met His Ser Asn Gln Gly Trp Arg Arg Val
 165 170 175
 Val Arg Ala Phe Lys Arg Val Gly Val Ser Arg Gln Ala Gln Ser Gly
 180 185 190
 Cys Val Lys Tyr Pro Ala Asx Pro Arg Trp Gly Arg Phe Ser Gly Ala
 195 200 205
 Ala Ala Pro Pro Asp Cys Trp Ser Asp
 210 215

<210> 38

<211> 217

<212> PRT

<213> Homosapiens

<220>

<223> Xaa= any amino acid

<223> Frame shift sequence

<223> Reverse strand

<400> 38

Met Gly Xaa Gly Pro Ile Cys Cys Xaa His Xaa Val Glu Trp Gly Pro
 1 5 10 15
 Pro Xaa Xaa Phe Lys Gly Trp Val Pro Gly Ala Arg Xaa Leu Lys Xaa
 20 25 30
 Pro Trp Ser Phe Glu Xaa Leu Pro Ala Leu Phe Cys Val Pro Leu Gly
 35 40 45
 Gln Asp Arg Xaa Asn Xaa Arg Val Pro Val Val Ile Xaa Arg Arg Ser
 50 55 60
 Xaa Pro Arg Val Phe Val Glu Val Arg Arg Gln Xaa Ala Leu Val Ser
 65 70 75 80
 Ser Ser Phe Ala Pro Leu His Gln Asp Val Leu Leu His Pro Asp Gln
 85 90 95
 Phe Leu Glu Phe Leu Arg Ile Leu Gln Leu Ala Val Leu Pro Val Arg
 100 105 110
 Gln Val Leu Ala Asn Pro Asp Pro Xaa Leu Gln His Arg Ser Lys Ala
 115 120 125
 Ser Ile Phe Ala Met Leu Ala Ser Ile Val Leu Val Ser Ala Thr Phe
 130 135 140
 Cys Thr Arg Cys Ser Ser Asp Ser Leu Ala Arg Cys Ser Glu Ser
 145 150 155 160
 Leu Arg Lys Tyr Ser Arg Cys Ile Arg Ile Lys Ala Gly Gly Val Ser
 165 170 175
 Ser Gly Lys Pro Ser Ser Ala Ser Val Phe Pro Ala Lys Arg Arg Ala
 180 185 190
 Val Ala Asn Thr Gln Gln Cys Arg Glu Lys Val Val Phe Gln Val Leu
 195 200 205
 Gln Leu Arg Leu Ile Ala Gly Arg Ile
 210 215

<210> 39

<211> 191

<212> DNA

<213> Homosapiens

<220>

<221> CDS

<222> (1)...(189)

<223> N= A,T,C or G

Xaa= any amino acid

<223> Synthetically generated nucleic acid

<400> 39

cgc gct gga cta tcn cta aag ggt ctc cna cna cgt cca ncc gga cna
 Arg Ala Gly Leu Ser Leu Lys Gly Leu Xaa Xaa Arg Pro Xaa Gly Xaa
 1 5 10 15

48

gct gac ctc gtt tcc ncn aag cgt gaa act gaa ggc cgg tga aac cnt
 Ala Asp Leu Val Ser Xaa Lys Arg Glu Thr Glu Gly Arg * Asn Xaa
 20 25 30

96

cnt gtt cgc ctn gat cac cta cta gtc gcg cgc cnn gcg cga cag gat
 Xaa Val Arg Leu Asp His Leu Leu Val Ala Arg Xaa Ala Arg Gln Asp
 35 40 45

144

caa cgc caa ggt gat ggc cga tcc ccg cct ggc gtc gtc gat gga
 Gln Arg Gln Gly Asp Gly Arg Ser Pro Pro Gly Val Val Asp Gly
 50 55 60

189

tc

<210> 40
<211> 62
<212> PRT
<213> Homosapiens

<220>
<223> Xaa= any amino acid

<223> Frame shift sequence

<400> 40
Arg Ala Gly Leu Ser Leu Lys Gly Leu Xaa Xaa Arg Pro Xaa Gly Xaa
 5 10 15
 1
Ala Asp Leu Val Ser Xaa Lys Arg Glu Thr Glu Gly Arg Asn Xaa Xaa
 20 25 30
Val Arg Leu Asp His Leu Leu Val Ala Arg Xaa Ala Arg Gln Asp Gln
 35 40 45
Arg Gln Gly Asp Gly Arg Ser Pro Pro Gly Val Val Asp Gly
 50 55 60

<210> 41
<211> 191
<212> DNA
<213> Homosapiens

<220>
<221> CDS
<222> (2)...(191)
<223> N= A,T,C or G
 Xaa= any amino acid

<223> Synthetically generated nucleic acid

<400> 41
c gcg ctg gac tat cnc taa agg gtc tcc nac nac gtc can ccg gac nag
 Ala Leu Asp Tyr Xaa * Arg Val Ser Xaa Xaa Val Xaa Pro Asp Xaa
 1 5 10 15

ctg acc tcg ttt ccn cna agc gtg aaa ctg aag gcc ggt gaa acc ntc
 Leu Thr Ser Phe Pro Xaa Ser Val Lys Leu Lys Ala Gly Glu Thr Xaa
 20 25 30

ntg ttc gcc tng atc acc tac tag tcg cgc gcc nng cgc gac agg atc
 Xaa Phe Ala Xaa Ile Thr Tyr * Ser Arg Ala Xaa Arg Asp Arg Ile
 35 40 45

aac gcc aag gtg atg gcc gat ccc cgc ctg gcg tcg tcg atg gat c
 Asn Ala Lys Val Met Ala Asp Pro Arg Leu Ala Ser Ser Met Asp
 50 55 60

49

97

145

191

<210> 42
<211> 61
<212> PRT
<213> Homosapiens

<220>
<223> Xaa= any amino acid

<223> Frame shift sequence

<400> 42

Ala	Leu	Asp	Tyr	Xaa	Arg	Val	Ser	Xaa	Xaa	Val	Xaa	Pro	Asp	Xaa	Leu
1				5					10					15	
Thr	Ser	Phe	Pro	Xaa	Ser	Val	Lys	Leu	Lys	Ala	Gly	Glu	Thr	Xaa	Xaa
				20				25				30			
Phe	Ala	Xaa	Ile	Thr	Tyr	Ser	Arg	Ala	Xaa	Arg	Asp	Arg	Ile	Asn	Ala
				35				40			45				
Lys	Val	Met	Ala	Asp	Pro	Arg	Leu	Ala	Ser	Ser	Met	Asp			
				50				55			60				

<210> 43

<211> 191

<212> DNA

<213> Homosapiens

<220>

<221> CDS

<222> (3) ... (191)

<223> N= A,T,C or G

Xaa= any amino acid

<223> Synthetically generated nucleic acid

<400> 43

cg	cgc	tgg	act	atc	nct	aaa	ggg	tct	ccn	acn	acg	tcc	anc	cgg	acn
Arg	Trp	Thr	Ile	Xaa	Lys	Gly	Ser	Pro	Thr	Thr	Ser	Xaa	Arg	Thr	
1				5					10				15		

agc	tga	cct	cgt	ttc	cnc	naa	gcg	tga	aac	tga	agg	ccg	gtg	aaa	ccn
Ser	*	Pro	Arg	Phe	Xaa	Xaa	Ala	*	Asn	*	Arg	Pro	Val	Lys	Pro
								20				25			

tcn	tgt	tcg	cct	nga	tca	cct	act	agt	cgc	gcf	ccn	ngc	gcf	aca	gga
Ser	Cys	Ser	Pro	Xaa	Ser	Pro	Thr	Ser	Arg	Ala	Pro	Xaa	Ala	Thr	Gly
30							35				40				

tca	acg	cca	agg	tga	tgg	ccg	atc	ccc	gcc	tgg	cgt	cgt	cga	tgg	atc
Ser	Thr	Pro	Arg	*	Trp	Pro	Ile	Pro	Ala	Trp	Arg	Arg	Arg	Trp	Ile
45					50					55					

<210> 44

<211> 59

<212> PRT

<213> Homosapiens

<220>

<223> Xaa= any amino acid

<223> Frame shift sequence

<400> 44

Arg	Trp	Thr	Ile	Xaa	Lys	Gly	Ser	Pro	Thr	Thr	Ser	Xaa	Arg	Thr	Ser
1					5				10				15		
Pro	Arg	Phe	Xaa	Xaa	Ala	Asn	Arg	Pro	Val	Lys	Pro	Ser	Cys	Ser	Pro
					20				25			30			
Xaa	Ser	Pro	Thr	Ser	Arg	Ala	Pro	Xaa	Ala	Thr	Gly	Ser	Thr	Pro	Arg
					35				40			45			

Trp Pro Ile Pro Ala Trp Arg Arg Arg Trp Ile
 50 55

<210> 45
<211> 190
<212> DNA
<213> Homosapiens

<220>
<223> N= A,T,C or G
<223> Synthetically generated nucleic acid
<223> Reverse strand

<400> 45				60
gatccatcga cgacgccagg cgggatcgac catcaccttg gcgttgcattc tgcgcgcnn				120
ggcgcgac tagtaggtga tcnaggcga cangangtt tcaccggct tcagttcac				180
gcttngngga aacgaggtca gctngtccgg ntggacgtng tnggagaccc tttagngata				190
gtccagcgcg				

<210> 46
<211> 61
<212> PRT
<213> Homosapiens

<220>
<223> Xaa= any amino acid
<223> Frame shift sequence
<223> Reverse strand

<400> 46				
Asp Pro Ser Thr Thr Pro Gly Gly Asp Arg Pro Ser Pro Trp Arg Ser				
1 5 10 15				
Cys Arg Xaa Xaa Arg Ala Thr Ser Arg Xaa Arg Arg Thr Xaa Xaa Phe				
20 25 30				
His Arg Pro Ser Val Ser Arg Xaa Xaa Glu Thr Arg Ser Ala Xaa Pro				
35 40 45				
Xaa Gly Arg Xaa Xaa Arg Pro Phe Xaa Asp Ser Pro Ala				
50 55 60				

<210> 47
<211> 63
<212> PRT
<213> Homosapiens

<220>
<223> Xaa= any amino acid
<223> Frame shift sequence
<223> Reverse strand

<400> 47				
Ile His Arg Arg Arg Gln Ala Gly Ile Gly His His Leu Gly Val Asp				
1 5 10 15				
Pro Val Ala Xaa Gly Ala Arg Leu Val Gly Asp Xaa Gly Glu Xaa Xaa				
20 25 30				
Gly Phe Thr Gly Leu Gln Phe His Ala Xaa Xaa Lys Arg Gly Gln Xaa				

35	40	45	
Val Arg Xaa Asp Xaa Xaa Gly Asp Pro Leu Xaa Ile Val Gln Arg			
50	55	60	
<210> 48			
<211> 59			
<212> PRT			
<213> Homosapiens			
<220>			
<223> Xaa= any amino acid			
<223> Frame shift sequence			
<223> Reverse strand			
<400> 48			
Ser Ile Asp Asp Ala Arg Arg Gly Ser Ala Ile Thr Leu Ala Leu Ile			
1	5	10	15
Leu Ser Arg Xaa Ala Arg Asp Val Ile Xaa Ala Asn Xaa Xaa Val Ser			
20	25	30	
Pro Ala Phe Ser Phe Thr Leu Xaa Gly Asn Glu Val Ser Xaa Ser Xaa			
35	40	45	
Trp Thr Xaa Xaa Glu Thr Leu Xaa Ser Ser Ala			
50	55		
<210> 49			
<211> 552			
<212> DNA			
<213> Homosapiens			
<220>			
<221> CDS			
<222> (1)...(552)			
<223> N= A,T,C or G			
Xaa= any amino acid			
<223> Synthetically generated nucleic acid			
<400> 49			
gat ccg ctc gat gcc cag gcc cag tac agc gaa ctg ttc gcc cat ggc			48
Asp Pro Leu Asp Ala Gln Ala Gln Tyr Ser Glu Leu Phe Ala His Gly			
1	5	10	15
cgc gcc acg tca ctg ttg cta ttc gaa cat gtt cac ggt gaa tcc cgt			96
Arg Ala Thr Ser Leu Leu Leu Phe Glu His Val His Gly Glu Ser Arg			
20	25	30	
gac cgc ggc cag gcg atg gtg gac ctg ctg gcg cag tac gag cag cac			144
Asp Arg Gly Gln Ala Met Val Asp Leu Leu Ala Gln Tyr Glu Gln His			
35	40	45	
ggt ttg cag tta aac agc cgc gaa tta ccg gac cac ctg ccg ctg tat			192
Gly Leu Gln Leu Asn Ser Arg Glu Leu Pro Asp His Leu Pro Leu Tyr			
50	55	60	
ctg gag tac ctg tcg cag ctg ccg caa ggc gaa gcc gtt gaa ggt ttg			240
Leu Glu Tyr Leu Ser Gln Leu Pro Gln Gly Glu Ala Val Glu Gly Leu			
65	70	75	80
aaa gat atc gcg ccg att ctg gca ttg ctg agc gcg cgt ctg caa cag			288

Lys Asp Ile Ala Pro Ile Leu Ala Leu Leu Ser Ala Arg Leu Gln Gln			
85	90	95	
cgt gaa agc cgt tat gcc gtg atg ttt gat ctg ctg ctg aaa ttg gcc		336	
Arg Glu Ser Arg Tyr Ala Val Met Phe Asp Leu Leu Lys Leu Ala			
100	105	110	
gat acc gct atc gac agc gac aaa gtg gcg gaa aaa att gcc gac gaa		384	
Asp Thr Ala Ile Asp Ser Asp Lys Val Ala Glu Lys Ile Ala Asp Glu			
115	120	125	
gcg cgc gat gat acg ccg cag gcg ctg gat gct gtt tgg gaa gaa gag		432	
Ala Arg Asp Asp Thr Pro Gln Ala Leu Asp Ala Val Trp Glu Glu Glu			
130	135	140	
cag gtt aaa ttc ttt gct gac aaa ggc tgc ggc gat tca gca atc act		480	
Gln Val Lys Phe Ala Asp Lys Gly Cys Gly Asp Ser Ala Ile Thr			
145	150	155	160
gct cat cag cgt cgc ttt gcc ggt gcc gtc gcg ccg caa tat ctg aat		528	
Ala His Gln Arg Arg Phe Ala Gly Ala Val Ala Pro Gln Tyr Leu Asn			
165	170	175	
atc ctc ggt gag agg ctg gag agt		552	
Ile Leu Gly Glu Arg Leu Glu Ser			
180			

<210> 50
<211> 184
<212> PRT
<213> Homosapiens

<220>
<223> Frame shift sequence

<223> Frame shift sequence

<400> 50
Asp Pro Leu Asp Ala Gln Ala Gln Tyr Ser Glu Leu Phe Ala His Gly
1 5 10 15
Arg Ala Thr Ser Leu Leu Leu Phe Glu His Val His Gly Glu Ser Arg
20 25 30
Asp Arg Gly Gln Ala Met Val Asp Leu Leu Ala Gln Tyr Glu Gln His
35 40 45
Gly Leu Gln Leu Asn Ser Arg Glu Leu Pro Asp His Leu Pro Leu Tyr
50 55 60
Leu Glu Tyr Leu Ser Gln Leu Pro Gln Gly Glu Ala Val Glu Gly Leu
65 70 75 80
Lys Asp Ile Ala Pro Ile Leu Ala Leu Leu Ser Ala Arg Leu Gln Gln
85 90 95
Arg Glu Ser Arg Tyr Ala Val Met Phe Asp Leu Leu Lys Leu Ala
100 105 110
Asp Thr Ala Ile Asp Ser Asp Lys Val Ala Glu Lys Ile Ala Asp Glu
115 120 125
Ala Arg Asp Asp Thr Pro Gln Ala Leu Asp Ala Val Trp Glu Glu Glu
130 135 140
Gln Val Lys Phe Phe Ala Asp Lys Gly Cys Gly Asp Ser Ala Ile Thr
145 150 155 160
Ala His Gln Arg Arg Phe Ala Gly Ala Val Ala Pro Gln Tyr Leu Asn
165 170 175

Ile Leu Gly Glu Arg Leu Glu Ser
180

<210> 51
<211> 552
<212> DNA
<213> Homosapiens

<220>
<221> CDS
<222> (2)...(552)
<223> N= A,T, C or G
Xaa= any amino acid

<223> Synthetically generated nucleic acid

<400> 51
g atc cgc tcg atg ccc agg ccc agt aca gcg aac tgt tcg ccc atg gcc 49
Ile Arg Ser Met Pro Arg Pro Ser Thr Ala Asn Cys Ser Pro Met Ala
1 5 10 15

gcg cca cgt cac tgt tgc tat tcg aac atg ttc acg gtg aat ccc gtg 97
Ala Pro Arg His Cys Cys Tyr Ser Asn Met Phe Thr Val Asn Pro Val
20 25 30

acc gcg gcc agg cga tgg tgg acc tgc tgg cgc agt acg agc agc acg 145
Thr Ala Ala Arg Arg Trp Trp Thr Cys Trp Arg Ser Thr Ser Ser Thr
35 40 45

gtt tgc agt taa aca gcc gcg aat tac cgg acc acc tgc cgc tgt atc 193
Val Cys Ser * Thr Ala Ala Asn Tyr Arg Thr Thr Cys Arg Cys Ile
50 55 60

tgg agt acc tgt cgc agc tgc cgc aag gcg aag ccg tgg aag gtt tga 241
Trp Ser Thr Cys Arg Ser Cys Arg Lys Ala Lys Pro Trp Lys Val *
65 70 75

aag ata tcg cgc cga ttc tgg cat tgc tga gcg cgc gtc tgc aac agc 289
Lys Ile Ser Arg Arg Phe Trp His Cys * Ala Arg Val Cys Asn Ser
80 85 90

gtg aaa gcc gtt atg ccg tga tgt ttg atc tgc tgc tga aat tgg ccg 337
Val Lys Ala Val Met Pro * Cys Leu Ile Cys Cys * Asn Trp Pro
95 100 105

ata ccg cta tcg aca gcg aca aag tgg cgg aaa aaa ttg ccg acg aag 385
Ile Pro Leu Ser Thr Ala Thr Lys Trp Arg Lys Lys Leu Pro Thr Lys
110 115 120

cgc gcg atg ata cgc cgc agg cgc tgg atg ctg ttt ggg aag aag agc 433
Arg Ala Met Ile Arg Arg Arg Trp Met Leu Phe Gly Lys Lys Ser
125 130 135

agg tta aat tct ttg ctg aca aag gct gcg gcg att cag caa tca ctg 481
Arg Leu Asn Ser Leu Leu Thr Lys Ala Ala Ile Gln Gln Ser Leu
140 145 150 155

ctc atc agc gtc gct ttg ccg gtg ccg tgc cgc cgc aat atc tga ata 529
Leu Ile Ser Val Ala Leu Pro Val Pro Ser Arg Arg Asn Ile * Ile
160 165 170

tcc tcg gtg aga ggc tgg aga gt
 Ser Ser Val Arg Gly Trp Arg
 175

<210> 52
 <211> 177
 <212> PRT
 <213> Homosapiens

<220>
 <223> Frame shift sequence

<400> 52
 Ile Arg Ser Met Pro Arg Pro Ser Thr Ala Asn Cys Ser Pro Met Ala
 1 5 10 15
 Ala Pro Arg His Cys Cys Tyr Ser Asn Met Phe Thr Val Asn Pro Val
 20 25 30
 Thr Ala Ala Arg Arg Trp Trp Thr Cys Trp Arg Ser Thr Ser Ser Thr
 35 40 45
 Val Cys Ser Thr Ala Ala Asn Tyr Arg Thr Thr Cys Arg Cys Ile Trp
 50 55 60
 Ser Thr Cys Arg Ser Cys Arg Lys Ala Lys Pro Trp Lys Val Lys Ile
 65 70 75 80
 Ser Arg Arg Phe Trp His Cys Ala Arg Val Cys Asn Ser Val Lys Ala
 85 90 95
 Val Met Pro Cys Leu Ile Cys Cys Asn Trp Pro Ile Pro Leu Ser Thr
 100 105 110
 Ala Thr Lys Trp Arg Lys Leu Pro Thr Lys Arg Ala Met Ile Arg
 115 120 125
 Arg Arg Arg Trp Met Leu Phe Gly Lys Lys Ser Arg Leu Asn Ser Leu
 130 135 140
 Leu Thr Lys Ala Ala Ala Ile Gln Gln Ser Leu Leu Ile Ser Val Ala
 145 150 155 160
 Leu Pro Val Pro Ser Arg Arg Asn Ile Ile Ser Ser Val Arg Gly Trp
 165 170 175
 Arg

<210> 53
 <211> 552
 <212> DNA
 <213> Homosapiens

<220>
 <221> CDS
 <222> (3)...(552)

<223> Synthetically generated nucleic acid

<400> 53
 ga tcc gct cga tgc cca ggc cca gta cag cga act gtt cgc cca tgg 47
 Ser Ala Arg Cys Pro Gly Pro Val Gln Arg Thr Val Arg Pro Trp
 1 5 10 15
 ccg cgc cac gtc act gtt gct att cga aca tgt tca cgg tga atc ccg 95
 Pro Arg His Val Thr Val Ala Ile Arg Thr Cys Ser Arg * Ile Pro
 20 25 30
 tga ccg cgg cca ggc gat ggt gga cct gct ggc gca gta cga gca gca
 * Pro Arg Pro Gly Asp Gly Pro Ala Gly Ala Val Arg Ala Ala 143

35

40

45

cggttt gca gtt aaa cag ccg cga att acc gga cca cct gcc gct gta Arg Phe Ala Val Lys Gln Pro Arg Ile Thr Gly Pro Pro Ala Ala Val	50	55	60	191
tct gga gta cct gtc gca gct gcc gca agg cga agc cgt gga agg ttt Ser Gly Val Pro Val Ala Ala Ala Arg Arg Ser Arg Gly Arg Phe	65	70	75	239
gaa aga tat cgc gcc gat tct ggc att gct gag cgc gcg tct gca aca Glu Arg Tyr Arg Ala Asp Ser Gly Ile Ala Glu Arg Ala Ser Ala Thr	80	85	90	287
gcg tga aag ccg tta tgc cgt gat gtt tga tct gct gct gaa att ggc Ala * Lys Pro Leu Cys Arg Asp Val * Ser Ala Ala Glu Ile Gly	95	100	105	335
cga tac cgc tat cga cag cga caa agt ggc gga aaa aat tgc cga cga Arg Tyr Arg Tyr Arg Gln Arg Gln Ser Gly Gly Lys Asn Cys Arg Arg	110	115	120	383
agc gcg cga tga tac gcc gca ggc gct gga tgc tgt ttg gga aga aga Ser Ala Arg * Tyr Ala Ala Gly Ala Gly Cys Cys Leu Gly Arg Arg	125	130	135	431
gca ggt taa att ctt tgc tga caa agg ctg cgg cga ttc agc aat cac Ala Gly * Ile Leu Cys * Gln Arg Leu Arg Arg Phe Ser Asn His	140	145	150	479
tgc tca tca gcg tcg ctt tgc cgg tgc cgt cgc gcc gca ata tct gaa Cys Ser Ser Ala Ser Leu Cys Arg Cys Arg Arg Ala Ala Ile Ser Glu	155	160	165	527
tat cct cgg tga gag gct gga gag t Tyr Pro Arg * Glu Ala Gly Glu	170	175		552

<210> 54
<211> 175
<212> PRT
<213> Homosapiens

<220>
<223> Frame shift sequence

<400> 54
Ser Ala Arg Cys Pro Gly Pro Val Gln Arg Thr Val Arg Pro Trp Pro
1 5 10 15
Arg His Val Thr Val Ala Ile Arg Thr Cys Ser Arg Ile Pro Pro Arg
20 25 30
Pro Gly Asp Gly Gly Pro Ala Gly Ala Val Arg Ala Ala Arg Phe Ala
35 40 45
Val Lys Gln Pro Arg Ile Thr Gly Pro Pro Ala Ala Val Ser Gly Val
50 55 60
Pro Val Ala Ala Ala Ala Arg Arg Ser Arg Gly Arg Phe Glu Arg Tyr
65 70 75 80
Arg Ala Asp Ser Gly Ile Ala Glu Arg Ala Ser Ala Thr Ala Lys Pro
85 90 95
Leu Cys Arg Asp Val Ser Ala Ala Glu Ile Gly Arg Tyr Arg Tyr Arg

100	105	110
Gln Arg Gln Ser Gly Gly Lys Asn Cys Arg Arg Ser Ala Arg Tyr Ala		
115	120	125
Ala Gly Ala Gly Cys Cys Leu Gly Arg Arg Ala Gly Ile Leu Cys Gln		
130	135	140
Arg Leu Arg Arg Phe Ser Asn His Cys Ser Ser Ala Ser Leu Cys Arg		
145	150	155
Cys Arg Arg Ala Ala Ile Ser Glu Tyr Pro Arg Glu Ala Gly Glu		
165	170	175

<210> 55
<211> 554
<212> DNA
<213> Homosapiens

<220>
<223> Synthetically generated nucleic acid

<223> Reverse strand

<400> 55	60
actctccagg ctctcaccga ggatattca gatattgcggc gcgacggcac cggcaaagcg	120
acgctgtatga gcagtgattt ctgaatcgcc gcagcctttg tcagcaaaga atttaacctg	180
ctcttcttcc caaacagcat ccagcgcctg cggcgtatca tcgcgcgc tt cgtcggcaat	240
ttttccgccc actttgtcgc tgtcgatagc aggttatcgg ccaatttcag caggagatca	300
aacatcacgg cataacggct ttcacgctgt tgca gagacgcg cgctcagcaa tgccagaatc	360
ggcgcgatata ttccaaacc ttccacggct tcgccttgcg gcagctgcga caggtactcc	420
agatatcagc ggcagggtggc cggtaattcg cggctgttta actgcaaacc gtgctgctcg	480
tactgcgcac gcagggtccac catgcgcctgg ccgcggtcac gggattcacc gtgaacatgt	540
tcaaatagca acagtgcac ggcgcggcca tggcgaaca gttcgctgta ctgggcctgg	554
gcatcgagcg gatc	

<210> 56
<211> 179
<212> PRT
<213> Homosapiens

<220>
<223> Frame shift sequence

<223> Reverse strand

<400> 56	
Thr Leu Gln Pro Leu Thr Glu Asp Ile Gln Ile Leu Arg Arg Asp Gly	
1 5 10 15	
Thr Gly Lys Ala Thr Leu Met Ser Ser Asp Cys Ile Ala Ala Ala Phe	
20 25 30	
Val Ser Lys Glu Phe Asn Leu Leu Phe Phe Pro Asn Ser Ile Gln Arg	
35 40 45	
Leu Arg Arg Ile Ile Ala Arg Phe Val Gly Asn Phe Phe Arg His Phe	
50 55 60	
Val Ala Val Asp Ser Gly Ile Gly Gln Phe Gln Gln Ile Lys His	
65 70 75 80	
His Gly Ile Thr Ala Phe Thr Leu Leu Gln Thr Arg Ala Gln Gln Cys	
85 90 95	
Gln Asn Arg Arg Asp Ile Phe Gln Arg Phe His Gly Phe Ala Leu Arg	
100 105 110	
Gln Leu Arg Gln Val Leu Gln Ile Gln Arg Gln Val Val Arg Arg Ala	
115 120 125	
Ala Val Leu Gln Thr Val Leu Leu Val Leu Arg Gln Gln Val His His	
130 135 140	

Arg Leu Ala Ala Val Thr Gly Phe Thr Val Asn Met Phe Glu Gln Gln
 145 150 155 160
 Arg Gly Ala Ala Met Gly Glu Gln Phe Ala Val Leu Gly Leu Gly Ile
 165 170 175
 Glu Arg Ile

<210> 57
<211> 179
<212> PRT
<213> Homosapiens

<220>
<223> Frame shift sequence

<223> Reverse strand

<400> 57
Leu Ser Ser Leu Ser Pro Arg Ile Phe Arg Tyr Cys Gly Ala Thr Ala
 1 5 10 15
Pro Ala Lys Arg Arg Ala Val Ile Ala Glu Ser Pro Gln Pro Leu Ser
 20 25 30
Ala Lys Asn Leu Thr Cys Ser Ser Gln Thr Ala Ser Ser Ala Cys
 35 40 45
Gly Val Ser Ser Arg Ala Ser Ser Ala Ile Phe Ser Ala Thr Leu Ser
 50 55 60
Leu Ser Ile Ala Val Ser Ala Asn Phe Ser Ser Arg Ser Asn Ile Thr
 65 70 75 80
Ala Arg Leu Ser Arg Cys Cys Arg Arg Ala Leu Ser Asn Ala Arg Ile
 85 90 95
Gly Ala Ile Ser Phe Lys Pro Ser Thr Ala Ser Pro Cys Gly Ser Cys
 100 105 110
Asp Arg Tyr Ser Arg Tyr Ser Gly Arg Trp Ser Gly Asn Ser Arg Leu
 115 120 125
Phe Asn Cys Lys Pro Cys Cys Ser Tyr Cys Ala Ser Arg Ser Thr Ile
 130 135 140
Ala Trp Pro Arg Ser Arg Asp Ser Pro Thr Cys Ser Asn Ser Asn Ser
 145 150 155 160
Asp Val Ala Arg Pro Trp Ala Asn Ser Ser Leu Tyr Trp Ala Trp Ala
 165 170 175
Ser Ser Gly

<210> 58
<211> 180
<212> PRT
<213> Homosapiens

<220>
<223> Frame shift sequence

<223> Reverse strand

<400> 58
Ser Pro Ala Ser His Arg Gly Tyr Ser Asp Ile Ala Ala Arg Arg His
 1 5 10 15
Arg Gln Ser Asp Ala Asp Glu Gln Leu Leu Asn Arg Arg Ser Leu Cys
 20 25 30
Gln Gln Arg Ile Pro Ala Leu Leu Pro Lys Gln His Pro Ala Pro Ala
 35 40 45
Ala Tyr His Arg Ala Leu Arg Arg Gln Phe Phe Pro Pro Leu Cys Arg

50	55	60
Cys Arg Arg Tyr Arg Pro Ile Ser Ala Ala Asp Gln Thr Ser Arg His		
65	70	75
Asn Gly Phe His Ala Val Ala Asp Ala Arg Ser Ala Met Pro Glu Ser		80
85	90	95
Ala Arg Tyr Leu Ser Asn Leu Pro Arg Leu Arg Leu Ala Ala Ala Ala		
100	105	110
Thr Gly Thr Pro Asp Thr Ala Ala Gly Gly Pro Val Ile Arg Gly Cys		
115	120	125
Leu Arg Ala Asn Arg Ala Ala Arg Thr Ala Pro Ala Gly Pro Pro Ser		
130	135	140
Pro Gly Arg Gly His Gly Ile His Arg Glu His Val Arg Ile Ala Thr		
145	150	155
Val Thr Trp Arg Gly His Gly Arg Thr Val Arg Cys Thr Gly Pro Gly		160
165	170	175
His Arg Ala Asp		
180		

<210> 59
<211> 265
<212> DNA
<213> Homosapiens

<220>
<221> CDS
<222> (1) ... (265)
<223> N= A, T, C or G
Xaa= any amino acid

<223> Synthetically generated nucleic acid

<400> 59	
gat cct nac aca nta gcc cgt gga cgc att tgc gtc gac cct cat ang	48
Asp Pro Xaa Thr Xaa Ala Arg Gly Arg Ile Cys Val Asp Pro His Xaa	
1	5
	10
	15
gaa gcg ata cga ggc ggg tna aag tga aca tcc gcc gag cac ggc agc	96
Glu Ala Ile Arg Gly Gly Xaa Lys * Thr Ser Ala Glu His Gly Ser	
20	25
	30
gac gcc tcc gct cac cgt cng cgc agt act tcc tcg ggt cgc cgc gcc	144
Asp Ala Ser Ala His Arg Xaa Arg Ser Thr Ser Gly Arg Arg Ala	
35	40
	45
tag cac tct gcg ccg tga cat caa ncc gtg aac cca cgg gag act ttg	192
* His Ser Ala Pro * His Gln Xaa Val Asn Pro Arg Glu Thr Leu	
50	55
	60
cgc cgc naa ggg atg agt cca cta tta gat gac gca tgg cta cga gcc	240
Arg Arg Xaa Gly Met Ser Pro Leu Leu Asp Asp Ala Trp Leu Arg Ala	
65	70
	75
nat cct cgg tga naa gct gga gag t	265
Xaa Pro Arg * Xaa Ala Gly Glu	
80	

<210> 60
<211> 84
<212> PRT
<213> Homosapiens

<220>

<223> Xaa= any amino acid

<223> Frame shift sequence

<400> 60

Asp	Pro	Xaa	Thr	Xaa	Ala	Arg	Gly	Arg	Ile	Cys	Val	Asp	Pro	His	Xaa
1				5					10					15	
Glu	Ala	Ile	Arg	Gly	Gly	Xaa	Lys	Thr	Ser	Ala	Glu	His	Gly	Ser	Asp
					20			25					30		
Ala	Ser	Ala	His	Arg	Xaa	Arg	Ser	Thr	Ser	Ser	Gly	Arg	Arg	Ala	His
					35			40				45			
Ser	Ala	Pro	His	Gln	Xaa	Val	Asn	Pro	Arg	Glu	Thr	Leu	Arg	Arg	Xaa
					50			55				60			
Gly	Met	Ser	Pro	Leu	Leu	Asp	Asp	Ala	Trp	Leu	Arg	Ala	Xaa	Pro	Arg
					65			70				75		80	
Xaa Ala Gly Glu															

<210> 61

<211> 265

<212> DNA

<213> Homosapiens

<220>

<221> CDS

<222> (2)...(265)

<223> N= A, T, C or G	
Xaa= any amino acid	

<223> Synthetically generated nucleic acid

<400> 61

g	atc	ctn	aca	can	tag	ccc	gtg	gac	gca	ttt	gcg	tcg	acc	ctc	ata	ngg
Ile	Leu	Thr	Xaa	*	Pro	Val	Asp	Ala	Phe	Ala	Ser	Thr	Leu	Ile	Xaa	
1					5				10					15		

aag	cga	tac	gag	gcg	ggt	naa	agt	gaa	cat	ccg	ccg	agc	acg	gca	gcg	
Lys	Arg	Tyr	Glu	Ala	Gly	Xaa	Ser	Glu	His	Pro	Pro	Ser	Thr	Ala	Ala	
						20			25				30			97

acg	cct	ccg	ctc	acc	gtc	ngc	gca	gta	ctt	cct	cg	gtc	gcc	gcg	cct	
Thr	Pro	Pro	Leu	Thr	Val	Xaa	Ala	Val	Leu	Pro	Arg	Val	Ala	Ala	Pro	
						35			40			45				145

agc	act	ctg	cgc	cgt	gac	atc	aan	ccg	tga	acc	cac	ggg	aga	ctt	tgc	
Ser	Thr	Leu	Arg	Arg	Asp	Ile	Xaa	Pro	*	Thr	His	Gly	Arg	Leu	Cys	
						50			55			60				193

gcc	gcn	aag	gga	tga	gtc	cac	tat	tag	atg	acg	cat	ggc	tac	gag	ccn	
Ala	Ala	Lys	Gly	*	Val	His	Tyr	*	Met	Thr	His	Gly	Tyr	Glu	Pro	
									65			70		75		

atc	ctc	ggt	gan	aag	ctg	gag	agt									265
Ile	Leu	Gly	Xaa	Lys	Leu	Glu	Ser									
							80									

<210> 62

<211> 84

<212> PRT
 <213> Homosapiens

<220>
 <223> Xaa=any amino acid

<223> Frame shift sequence

<400> 62
 Ile Leu Thr Xaa Pro Val Asp Ala Phe Ala Ser Thr Leu Ile Xaa Lys
 1 5 10 15
 Arg Tyr Glu Ala Gly Xaa Ser Glu His Pro Pro Ser Thr Ala Ala Thr
 20 25 30
 Pro Pro Leu Thr Val Xaa Ala Val Leu Pro Arg Val Ala Ala Pro Ser
 35 40 45
 Thr Leu Arg Arg Asp Ile Xaa Pro Thr His Gly Arg Leu Cys Ala Ala
 50 55 60
 Lys Gly Val His Tyr Met Thr His Gly Tyr Glu Pro Ile Leu Gly Xaa
 65 70 75 80
 Lys Leu Glu Ser

<210> 63
 <211> 265
 <212> DNA
 <213> Homosapiens

<220>
 <221> CDS
 <222> (3)...(265)
 <223> N= A, T, C or G
 Xaa= any amino acid

<223> Frame shift sequence

<400> 63
 ga tcc tna cac ant agc ccg tgg acg cat ttg cgt cga ccc tca tan 47
 Ser Xaa His Xaa Ser Pro Trp Thr His Leu Arg Arg Pro Ser Xaa
 1 5 10 15
 gga agc gat acg agg cgg gtn aaa gtg aac atc cgc cga gca cgg cag 95
 Gly Ser Asp Thr Arg Arg Val Lys Val Asn Ile Arg Arg Ala Arg Gln
 20 25 30
 cga cgc ctc cgc tca ccg tcn gcg cag tac ttc ctc ggg tcg ccc cgc 143
 Arg Arg Leu Arg Ser Pro Ser Ala Gln Tyr Phe Leu Gly Ser Pro Arg
 35 40 45
 cta gca ctc tgc gcc gtg aca tca anc cgt gaa ccc acg gga gac ttt 191
 Leu Ala Leu Cys Ala Val Thr Ser Xaa Arg Glu Pro Thr Gly Asp Phe
 50 55 60
 gcg ccg cna agg gat gag tcc act att aga tga cgc atg gct acg agc 239
 Ala Pro Xaa Arg Asp Glu Ser Thr Ile Arg * Arg Met Ala Thr Ser
 65 70 75
 cna tcc tcg gtg ana agc tgg aga gt 265
 Xaa Ser Ser Val Xaa Ser Trp Arg
 80 85

<210> 64
<211> 86
<212> PRT
<213> Homosapiens

<220>
<223> Xaa=any amino acid
<223> Frame shift sequence

<400> 64
Ser Xaa His Xaa Ser Pro Trp Thr His Leu Arg Arg Pro Ser Xaa Gly
1 5 10 15
Ser Asp Thr Arg Arg Val Lys Val Asn Ile Arg Arg Ala Arg Gln Arg
20 25 30
Arg Leu Arg Ser Pro Ser Ala Gln Tyr Phe Leu Gly Ser Pro Arg Leu
35 40 45
Ala Leu Cys Ala Val Thr Ser Xaa Arg Glu Pro Thr Gly Asp Phe Ala
50 55 60
Pro Xaa Arg Asp Glu Ser Thr Ile Arg Arg Met Ala Thr Ser Xaa Ser
65 70 75 80
Ser Val Xaa Ser Trp Arg
85

<210> 65
<211> 265
<212> DNA
<213> Homosapiens

<220>
<223> N= A, T, C or G

<223> Synthetically generated nucleic acid

<223> Reverse strand

<400> 65
actctccagc ttntcaccga ggatnggctc gtagccatgc gtcatcta at agtggactca 60
tcccttngcg gcgaaagt c tcccgtgggt tcacggntt g atgtcacggc gcagagtgc 120
aggcgccggcg acccgaggaa gtactgcgcn gacggtgagc ggaggcgtcg ctgccgtgc 180
cggcggatgt tcacttnac ccgcctcgta tcgcttccnt atgagggtcg acgcaa atgc 240
gtccacgggc tantgtgtna ggatc 265

<210> 66
<211> 88
<212> PRT
<213> Homosapiens

<220>
<223> Xaa= any amino acid

<223> Frame shift sequence

<223> Reverse strand

<400> 66
Thr Leu Gln Leu Xaa Thr Glu Asp Xaa Leu Val Ala Met Arg His Leu
1 5 10 15
Ile Val Asp Ser Ser Leu Xaa Gly Ala Lys Ser Pro Val Gly Ser Arg
20 25 30

Xaa Asp Val Thr Ala Gln Ser Ala Arg Arg Gly Asp Pro Arg Lys Tyr
 35 40 45
 Cys Xaa Asp Gly Glu Arg Arg Arg Arg Cys Arg Ala Arg Arg Met Phe
 50 55 60
 Thr Xaa Thr Arg Leu Val Ser Leu Xaa Tyr Glu Gly Arg Arg Lys Cys
 65 70 75 80
 Val His Gly Leu Xaa Cys Xaa Asp
 85

<210> 67

<211> 85

<212> PRT

<213> Homosapiens

<220>

<223> Xaa= any amino acid

<223> Frame shift sequence

<223> Reverse strand

<400> 67

Leu Ser Ser Xaa Ser Pro Arg Xaa Gly Ser Pro Cys Val Ile Trp Thr
 1 5 10 15
 His Pro Xaa Ala Ala Gln Ser Leu Pro Trp Val His Xaa Leu Met Ser
 20 25 30
 Arg Arg Arg Val Leu Gly Ala Ala Thr Arg Gly Ser Thr Ala Xaa Thr
 35 40 45
 Val Ser Gly Gly Val Ala Ala Val Leu Gly Gly Cys Ser Leu Xaa Pro
 50 55 60
 Ala Ser Tyr Arg Phe Xaa Met Arg Val Asp Ala Asn Ala Ser Thr Gly
 65 70 75 80
 Xaa Cys Xaa Arg Ile
 85

<210> 68

<211> 83

<212> PRT

<213> Homosapiens

<220>

<223> Xaa= any amino acid

<223> Frame shift sequence

<223> Reverse strand

<400> 68

Ser Pro Ala Xaa His Arg Gly Xaa Ala Arg Ser His Ala Ser Ser Asn
 1 5 10 15
 Ser Gly Leu Ile Pro Xaa Arg Arg Lys Val Ser Arg Gly Phe Thr Xaa
 20 25 30
 Cys His Gly Ala Glu Cys Ala Arg Arg Pro Glu Glu Val Leu Arg Xaa
 35 40 45
 Arg Ala Glu Ala Ser Leu Pro Cys Ser Ala Asp Val His Phe Xaa Pro
 50 55 60
 Pro Arg Ile Ala Ser Xaa Gly Ser Thr Gln Met Arg Pro Arg Ala Xaa
 65 70 75 80
 Val Xaa Gly

<210> 69
<211> 317
<212> DNA
<213> Homosapiens

<220>
<221> CDS
<222> (1)...(317)
<223> N= A, T, C or G
Xaa= any amino acid

<223> Synthetically generated nucleic acid

<400> 69		48
gat ccg gcc ncg cac gan ctt acc ggt naa aac ttc cnc ncc nat aat		
Asp Pro Ala Xaa His Xaa Leu Thr Gly Xaa Asn Phe Xaa Xaa Xaa Asn		
1 5 10 15		
att tgc cgc gcg agc cgc cct gan gct ctc ggc gta act ccg gat gca		96
Ile Cys Arg Ala Ser Arg Pro Xaa Ala Leu Gly Val Thr Pro Asp Ala		
20 25 30		
cgg ggg acc gtg acg gtt gta ntg ccc tgg ctt ttc tca gcn gaa atc		144
Arg Gly Thr Val Thr Val Val Xaa Pro Trp Leu Phe Ser Ala Glu Ile		
35 40 45		
tgc aca gcc atc ttc cga tcg atc tgg cgc agg tgg ggc ggc nca aaa		192
Cys Thr Ala Ile Phe Arg Ser Ile Trp Arg Arg Trp Gly Gly Xaa Lys		
50 55 60		
cgg tgg gca tct cca aac cgc agg aac gtg ttt tgc agg atg tcg aac		240
Arg Trp Ala Ser Pro Asn Arg Arg Asn Val Phe Cys Arg Met Ser Asn		
65 70 75 80		
atc atc cac gct tcg gtn ccc aac ggc tac ttc gcc cggt tac cggt ggc		288
Ile Ile His Ala Ser Val Pro Asn Gly Tyr Phe Ala Arg Tyr Arg Ala		
85 90 95		
atg tca tcc tcg gtg ana agc tgg ana nt		317
Met Ser Ser Ser Val Xaa Ser Trp Xaa		
100 105		

<210> 70
<211> 105
<212> PRT
<213> Homosapiens

<220>
<223> Xaa= any amino acid

<223> Frame shift sequence

<400> 70						
Asp Pro Ala Xaa His Xaa Leu Thr Gly Xaa Asn Phe Xaa Xaa Xaa Asn						
1 5 10 15						
Ile Cys Arg Ala Ser Arg Pro Xaa Ala Leu Gly Val Thr Pro Asp Ala						
20 25 30						
Arg Gly Thr Val Thr Val Val Xaa Pro Trp Leu Phe Ser Ala Glu Ile						
35 40 45						
Cys Thr Ala Ile Phe Arg Ser Ile Trp Arg Arg Trp Gly Gly Xaa Lys						

50	55	60
Arg Trp Ala Ser Pro Asn Arg Arg Asn Val Phe Cys Arg Met Ser Asn		
65	70	75
Ile Ile His Ala Ser Val Pro Asn Gly Tyr Phe Ala Arg Tyr Arg Ala		80
	85	90
Met Ser Ser Ser Val Xaa Ser Trp Xaa		95
	100	105

<210> 71
<211> 317
<212> DNA
<213> Homosapiens

<220>
<221> CDS
<222> (2)...(317)
<223> N= A, T, C or G
Xaa= any amino acid

<223> Synthetically generated nucleic acid

<400> 71
g atc cgg ccn cgc acg anc tta ccg gtn aaa act tcc ncn ccn ata ata 49
Ile Arg Pro Arg Thr Xaa Leu Pro Val Lys Thr Ser Xaa Pro Ile Ile
1 5 10 15

ttt gcc gcg cga gcc ctg ang ctc tcg gcg taa ctc cgg atg cac 97
Phe Ala Ala Arg Ala Ala Leu Xaa Leu Ser Ala * Leu Arg Met His
20 25 30

ggg gga ccg tga cgg ttg tan tgc cct ggc ttt tct cag cng aaa tct 145
Gly Gly Pro * Arg Leu Xaa Cys Pro Gly Phe Ser Gln Xaa Lys Ser
35 40 45

gca cag cca tct tcc gat cga tct ggc gca ggt ggg gcg gcn caa aac 193
Ala Gln Pro Ser Ser Asp Arg Ser Gly Ala Gly Ala Ala Gln Asn
50 55 60

ggt ggg cat ctc caa acc gca gga acg tgt ttt gca gga tgt cga aca 241
Gly Gly His Leu Gln Thr Ala Gly Thr Cys Phe Ala Gly Cys Arg Thr
65 70 75

tca tcc acg ctt cgg tnc cca acg gct act tcg ccc ggt acc ggg cca 289
Ser Ser Thr Leu Arg Xaa Pro Thr Ala Thr Ser Pro Gly Thr Gly Pro
80 85 90

tgt cat cct cgg tga naa gct gga nan t 317
Cys His Pro Arg * Xaa Ala Gly Xaa
95 100

<210> 72
<211> 102
<212> PRT
<213> Homosapiens

<220>
<223> Xaa= any amino acid

<223> Frame shift sequence

<400> 72
 Ile Arg Pro Arg Thr Xaa Leu Pro Val Lys Thr Ser Xaa Pro Ile Ile
 1 5 10 15
 Phe Ala Ala Arg Ala Ala Leu Xaa Leu Ser Ala Leu Arg Met His Gly
 20 25 30
 Gly Pro Arg Leu Xaa Cys Pro Gly Phe Ser Gln Xaa Lys Ser Ala Gln
 35 40 45
 Pro Ser Ser Asp Arg Ser Gly Ala Gly Gly Ala Ala Gln Asn Gly Gly
 50 55 60
 His Leu Gln Thr Ala Gly Thr Cys Phe Ala Gly Cys Arg Thr Ser Ser
 65 70 75 80
 Thr Leu Arg Xaa Pro Thr Ala Thr Ser Pro Gly Thr Gly Pro Cys His
 85 90 95
 Pro Arg Xaa Ala Gly Xaa
 100

<210> 73

<211> 317

<212> DNA

<213> Homosapiens

<220>

<221> CDS

<222> (3) ... (317)

<223> N= A, T, C or G

Xaa= any amino acid

<223> Synthetically generated nucleic acid

<400> 73

ga tcc ggc cnc gca cga nct tac cggt tna aaa ctt ccn cnc cna taa 47
 Ser Gly Xaa Ala Arg Xaa Tyr Arg Xaa Lys Leu Pro Xaa Xaa *
 1 5 10

tat ttg ccg cgc gag ccg ccc tga ngc tct cggt aac tcc gga tgc 95
 Tyr Leu Pro Arg Glu Pro Pro * Xaa Ser Arg Arg Asn Ser Gly Cys
 15 20 25

acg ggg gac cgt gac ggt tgt ant gcc ctg gct ttt ctc agc nga aat 143
 Thr Gly Asp Arg Asp Gly Cys Xaa Ala Leu Ala Phe Leu Ser Xaa Asn
 30 35 40 45

ctg cac agc cat ctt ccg atc gat ctg gcg cag gtg ggg cgg cnc aaa 191
 Leu His Ser His Leu Pro Ile Asp Leu Ala Gln Val Gly Arg Xaa Lys
 50 55 60

acg gtg ggc atc tcc aaa ccg cag gaa cgt gtt ttg cag gat gtc gaa 239
 Thr Val Gly Ile Ser Lys Pro Gln Glu Arg Val Leu Gln Asp Val Glu
 65 70 75

cat cat cca cgc ttc ggt ncc caa ccg cta ctt cgc ccg gta ccc ggc 287
 His His Pro Arg Phe Gly Xaa Gln Arg Leu Leu Arg Pro Val Pro Gly
 80 85 90

cat gtc atc ctc ggt gan aag ctg gan ant 317
 His Val Ile Leu Gly Xaa Lys Leu Xaa Xaa
 95 100

<210> 74

<211> 103

<212> PRT
<213> Homosapiens

<220>
<223> Xaa= any amino acid

<223> Frame shift sequence

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<400> 74
Ser Gly Xaa Ala Arg Xaa Tyr Arg Xaa Lys Leu Pro Xaa Xaa Tyr Leu
      5          10          15
    1
Pro Arg Glu Pro Pro Xaa Ser Arg Arg Asn Ser Gly Cys Thr Gly Asp
      20          25          30
Arg Asp Gly Cys Xaa Ala Leu Ala Phe Leu Ser Xaa Asn Leu His Ser
      35          40          45
His Leu Pro Ile Asp Leu Ala Gln Val Gly Arg Xaa Lys Thr Val Gly
      50          55          60
Ile Ser Lys Pro Gln Glu Arg Val Leu Gln Asp Val Glu His His Pro
      65          70          75          80
Arg Phe Gly Xaa Gln Arg Leu Leu Arg Pro Val Pro Gly His Val Ile
      85          90          95
Leu Gly Xaa Lys Leu Xaa Xaa
      100

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<210> 75

<211> 316

<212> DNA

<213> Homosapiens

<220>

<223> N= A, T, C or G

<223> Synthetically generated nucleic acid

<223> Reverse strand

<400> 75

antntccagg ttntcaccgga ggatgacatg gcccggtaacc gggcgaagta gccgttgggn
accgaagcgt ggatgtatgtt cgacatcctg caaaaacacgt tcctgcggtt tggagatgcc
caccgttttg ngccgccccac ctgcgccaga tcgatcgaa gatggctgtg cagatttcng
ctgagaaaag ccagggcant acaaccgtca cggtcccccg tgcacccgga gttacccgca
gagcntcagg ggggctcgcg cgccaaatat tatnggngng gaagttttna ccggtaagnt
cgtgcgnggc cggatc

60
120
180
240
300
316

<210> 76

<211> 104

<212> PRT

<213> Homosapiens

<220>

<223> Xaa= any amino acid

<223> Frame shift sequence

<223> Reverse strand

<400> 76

Phe Leu Arg Phe Gly Asp Ala His Arg Phe Xaa Pro Pro His Leu Arg
 35 40 45
 Gln Ile Asp Arg Lys Met Ala Val Gln Ile Xaa Ala Glu Lys Ser Gln
 50 55 60
 Gly Xaa Thr Thr Val Thr Val Pro Arg Ala Ser Gly Val Thr Pro Arg
 65 70 75 80
 Xaa Ser Gly Arg Leu Ala Arg Gln Ile Leu Xaa Xaa Xaa Lys Phe Xaa
 85 90 95
 Pro Val Xaa Ser Cys Xaa Ala Gly
 100

B1
long.

<210> 77

<211> 103

<212> PRT

<213> Homosapiens

<220>

<223> Xaa= any amino acid

<223> Frame shift sequence

<223> Reverse strand

<400> 77

Xaa Ser Ser Xaa Ser Pro Arg Met Thr Trp Pro Gly Thr Gly Arg Ser
 1 5 10 15
 Ser Arg Trp Xaa Pro Lys Arg Gly Cys Ser Thr Ser Cys Lys Thr Arg
 20 25 30
 Ser Cys Gly Leu Arg Met Pro Thr Val Leu Xaa Arg Pro Thr Cys Ala
 35 40 45
 Arg Ser Ile Gly Arg Trp Leu Cys Arg Phe Xaa Leu Arg Lys Ala Arg
 50 55 60
 Ala Xaa Gln Pro Ser Arg Ser Pro Val His Pro Glu Leu Arg Arg Glu
 65 70 75 80
 Xaa Gln Gly Gly Ser Arg Gly Lys Tyr Tyr Xaa Xaa Gly Ser Phe Xaa
 85 90 95
 Arg Xaa Arg Ala Xaa Pro Asp
 100

<210> 78

<211> 103

<212> PRT

<213> Homosapiens

<220>

<223> Xaa= any amino acid

<223> Frame shift sequence

<223> Reverse strand

<400> 78

Xaa Pro Ala Xaa His Arg Gly His Gly Pro Val Pro Gly Glu Val Ala
 1 5 10 15
 Val Gly Xaa Arg Ser Val Asp Asp Val Arg His Pro Ala Lys His Val
 20 25 30
 Pro Ala Val Trp Arg Cys Pro Pro Phe Xaa Ala Ala Pro Pro Ala Pro
 35 40 45
 Asp Arg Ser Glu Asp Gly Cys Ala Asp Phe Xaa Glu Lys Pro Gly Xaa
 50 55 60
 Tyr Asn Arg His Gly Pro Pro Cys Ile Arg Ser Tyr Ala Glu Ser Xaa

65	70	75	80
Arg Ala Ala Arg Ala Ala Asn Ile Xaa Xaa Xaa Glu Val Xaa Thr Gly			
85	90	95	
Lys Xaa Val Xaa Gly Arg Ile			
100			

<210> 79

<211> 341

<212> DNA

<213> Homosapiens

<220>

<221> CDS

<222> (1)...(341)

<223> N= A, T, C or G

Xaa= any amino acid

<223> Synthetically generated nucleic acid

<400> 79	48		
act ctc cag cct cgc acc gag gat cag ggc gtc gtc gac tcc gtc gac			
Thr Leu Gln Pro Arg Thr Glu Asp Gln Gly Val Val Asp Ser Val Asp			
1	5	10	15

ctg acc gcc tcc ccn ccg ctg ctc tcg atc ggc ggc cag acc tac acc	96		
Leu Thr Ala Ser Pro Pro Leu Leu Ser Ile Gly Gly Gln Thr Tyr Thr			
20	25	30	

anc gac gta gat caa gcg cgt ggt gcg cgg cgc nac nag can can cta	144		
Xaa Asp Val Asp Gln Ala Arg Gly Ala Arg Arg Xaa Xaa Xaa Xaa Leu			
35	40	45	

ant caa ggc ctc gct gca tcc cgc caa tcc agc gct cag ctt cgc ggg	192		
Xaa Gln Gly Leu Ala Ala Ser Arg Gln Ser Ser Ala Gln Leu Arg Gly			
50	55	60	

aat tgc gcg anc gct ttt gcg cgt cnc gag tna ccg cat aca cac ctg	240		
Asn Cys Ala Xaa Ala Phe Ala Arg Xaa Glu Xaa Pro His Thr His Leu			
65	70	75	80

ccg tcc ctg cga aag caa gga ccc ata ctc cgc ngc ggg tgt tgt tga	288		
Pro Ser Leu Arg Lys Gln Gly Pro Ile Leu Arg Xaa Gly Cys Cys *			
85	90	95	

cgg gac tcg tca tgg cgg caa cgc aca acg tnn aac ttc tgt ggt tat	336		
Arg Asp Ser Ser Trp Arg Gln Arg Thr Thr Xaa Asn Phe Cys Gly Tyr			
100	105	110	

gga tc

Gly

<210> 80

<211> 112

<212> PRT

<213> Homosapiens

<220>

<223> Xaa= any amino acid

<223> Frame shift sequence

<400> 80
 Thr Leu Gln Pro Arg Thr Glu Asp Gln Gly Val Val Asp Ser Val Asp
 1 5 10 15
 Leu Thr Ala Ser Pro Pro Leu Leu Ser Ile Gly Gly Gln Thr Tyr Thr
 20 25 30
 Xaa Asp Val Asp Gln Ala Arg Gly Ala Arg Arg Xaa Xaa Xaa Xaa Leu
 35 40 45
 Xaa Gln Gly Leu Ala Ala Ser Arg Gln Ser Ser Ala Gln Leu Arg Gly
 50 55 60
 Asn Cys Ala Xaa Ala Phe Ala Arg Xaa Glu Xaa Pro His Thr His Leu
 65 70 75 80
 Pro Ser Leu Arg Lys Gln Gly Pro Ile Leu Arg Xaa Gly Cys Cys Arg
 85 90 95
 Asp Ser Ser Trp Arg Gln Arg Thr Thr Xaa Asn Phe Cys Gly Tyr Gly
 100 105 110

<210> 81
<211> 341
<212> DNA
<213> Homosapiens

<220>
<221> CDS
<222> (2)...(341)
<223> N= A, T, C or G
Xaa= any amino acid

<223> Synthetically generated nucleic acid

<400> 81
 a ctc tcc agc ctc gca ccg agg atc agg gcg tcg tcg act ccg tcg acc 49
 Leu Ser Ser Leu Ala Pro Arg Ile Arg Ala Ser Ser Thr Pro Ser Thr
 1 5 10 15
 tga ccg cct ccc cnc cgc tgc tct cga tcg gcg gcc aga cct aca cca 97
 * Pro Pro Pro Xaa Arg Cys Ser Arg Ser Ala Ala Arg Pro Thr Pro
 20 25 30
 ncg acg tag atc aag cgc gtg gtg cgc ggc gcn acn agc anc anc taa 145
 Xaa Thr * Ile Lys Arg Val Val Arg Gly Ala Thr Ser Xaa Xaa *
 35 40 45
 ntc aag gcc tcg ctg cat ccc gcc aat cca gcg ctc agc ttc gcg gga 193
 Xaa Lys Ala Ser Leu His Pro Ala Asn Pro Ala Leu Ser Phe Ala Gly
 50 55 60
 att gcg cga ncg ctt ttg cgc gtc ncg agt nac cgc ata cac acc tgc 241
 Ile Ala Arg Xaa Leu Leu Arg Val Xaa Ser Xaa Arg Ile His Thr Cys
 65 70 75
 cgt ccc tgc gaa agc aag gac cca tac tcc gcn gcg ggt gtt gtt gac 289
 Arg Pro Cys Glu Ser Lys Asp Pro Tyr Ser Ala Ala Gly Val Val Asp
 80 85 90
 ggg act cgt cat ggc ggc aac gca caa cgt nna act tct gtg gtt atg 337
 Gly Thr Arg His Gly Gly Asn Ala Gln Arg Xaa Thr Ser Val Val Met
 95 100 105
 gat c 341

Asp
110

<210> 82
<211> 110
<212> PRT
<213> Homosapiens

<220>
<223> Xaa= any amino acid

<223> Frame shift sequence

<400> 82
Leu Ser Ser Leu Ala Pro Arg Ile Arg Ala Ser Ser Thr Pro Ser Thr
1 5 10 15
Pro Pro Pro Xaa Arg Cys Ser Arg Ser Ala Ala Arg Pro Thr Pro Xaa
20 25 30
Thr Ile Lys Arg Val Val Arg Gly Ala Thr Ser Xaa Xaa Xaa Lys Ala
35 40 45
Ser Leu His Pro Ala Asn Pro Ala Leu Ser Phe Ala Gly Ile Ala Arg
50 55 60
Xaa Leu Leu Arg Val Xaa Ser Xaa Arg Ile His Thr Cys Arg Pro Cys
65 70 75 80
Glu Ser Lys Asp Pro Tyr Ser Ala Ala Gly Val Val Asp Gly Thr Arg
85 90 95
His Gly Gly Asn Ala Gln Arg Xaa Thr Ser Val Val Met Asp
100 105 110

<210> 83
<211> 341
<212> DNA
<213> Homosapiens

<220>
<221> CDS
<222> (3)...(341)
<223> N= A, T, C or G
Xaa= any amino acid

<223> Synthetically generated nucleic acid

<400> 83 ac tct cca gcc tcg cac cga gga tca ggg cgt cgt cga ctc cgt cga 1 5 10 15	47
Ser Pro Ala Ser His Arg Gly Ser Gly Arg Arg Arg Leu Arg Arg	
cct gac cgc ctc ccc ncc gct gct ctc gat cgg cgg cca gac cta cac 20 25 30	95
Pro Asp Arg Leu Pro Xaa Ala Ala Leu Asp Arg Arg Pro Asp Leu His	
can cga cgt aga tca agc gcg tgg tgc gcg gcg cna cna gca nca nct 35 40 45	143
Xaa Arg Arg Arg Ser Ser Ala Trp Cys Ala Ala Xaa Xaa Xaa Xaa	
aan tca agg cct cgc tgc atc ccg cca atc cag cgc tca gct tcg cgg 50 55 60	191
Xaa Ser Arg Pro Arg Cys Ile Pro Pro Ile Gln Arg Ser Ala Ser Arg	
gaa ttg cgc gan cgc ttt tgc gcg tcn cga gtn acc gca tac aca cct	239

Glu Leu Arg Xaa Arg Phe Cys Ala Ser Arg Val Thr Ala Tyr Thr Pro
 65 70 75

gcc gtc cct gcg aaa gca agg acc cat act ccg cng cgg gtg ttg ttg
 Ala Val Pro Ala Lys Ala Arg Thr His Thr Pro Xaa Arg Val Leu Leu 287
 80 85 90 95

acg gga ctc gtc atg gcg gca acg cac aac gtn naa ctt ctg tgg tta
 Thr Gly Leu Val Met Ala Ala Thr His Asn Val Xaa Leu Leu Trp Leu 335
 100 105 110

tgg atc
 Trp Ile 341

<210> 84
 <211> 113
 <212> PRT
 <213> Homosapiens

<220>
 <223> Xaa= any amino acid

<223> Frame shift sequence

<400> 84
 Ser Pro Ala Ser His Arg Gly Ser Gly Arg Arg Arg Leu Arg Arg Pro
 1 5 10 15
 Asp Arg Leu Pro Xaa Ala Ala Leu Asp Arg Arg Pro Asp Leu His Xaa
 20 25 30
 Arg Arg Arg Ser Ser Ala Trp Cys Ala Ala Xaa Xaa Ala Xaa Xaa Xaa
 35 40 45
 Ser Arg Pro Arg Cys Ile Pro Pro Ile Gln Arg Ser Ala Ser Arg Glu
 50 55 60
 Leu Arg Xaa Arg Phe Cys Ala Ser Arg Val Thr Ala Tyr Thr Pro Ala
 65 70 75 80
 Val Pro Ala Lys Ala Arg Thr His Thr Pro Xaa Arg Val Leu Leu Thr
 85 90 95
 Gly Leu Val Met Ala Ala Thr His Asn Val Xaa Leu Leu Trp Leu Trp
 100 105 110
 Ile

<210> 85
 <211> 342
 <212> DNA
 <213> Homosapiens

<220>
 <223> N= A, T, C or G

<223> synthetically generated nucleic acid

<223> Reverse strand

<400> 85
 gatccataac cacagaagtt nnacgttgtc cgttggcgcc atgacgagtc ccgtcaacaa 60
 cacccgcngc ggagtatggg tccttgctt cgcaggacg gcaggtgtt atgcggtnac 120
 tcgngacgca caaaagcgnt cgcgcaattc ccgcgaagct gagcgcgtgg attggcgaaa 180
 tgcagcggagg ccttgantta gntgntgctn gtngcgccgc gcaccacgca cttgatctac 240

gtcgntggc taggtctggc cgccgatcga gagcagcgg ggggaggcgg tcaggtcgac 300
 ggagtgcacg acgcctgat ctcggtgcg aggctggaga gt 342

<210> 86
 <211> 107
 <212> PRT
 <213> Homosapiens

<220>
 <223> Xaa= any amino acid
 <223> Frame shift sequence
 <223> Reverse strand

<400> 86
 Asp Pro Pro Gln Lys Xaa Xaa Val Val Arg Cys Arg His Asp Glu Ser
 1 5 10 15
 Arg Gln Gln His Pro Xaa Arg Ser Met Gly Pro Cys Phe Arg Arg Asp
 20 25 30
 Gly Arg Cys Val Cys Gly Xaa Ser Xaa Arg Ala Lys Ala Xaa Ala Gln
 35 40 45
 Phe Pro Arg Ser Ala Leu Asp Trp Arg Asp Ala Ala Arg Pro Xaa Xaa
 50 55 60
 Xaa Cys Xaa Xaa Arg Arg Ala Pro Arg Ala Ser Thr Ser Xaa Val Val
 65 70 75 80
 Trp Pro Pro Ile Glu Ser Ser Xaa Gly Glu Ala Val Arg Ser Thr Glu
 85 90 95
 Ser Thr Thr Pro Ser Ser Val Arg Gly Trp Arg
 100 105

<210> 87
 <211> 113
 <212> PRT
 <213> Homosapiens

<220>
 <223> Xaa= any amino acid
 <223> Frame shift sequence
 <223> Reverse strand

<400> 87
 Ile His Asn His Arg Ser Xaa Thr Leu Cys Val Ala Ala Met Thr Ser
 1 5 10 15
 Pro Val Asn Asn Thr Arg Xaa Gly Val Trp Val Leu Ala Phe Ala Gly
 20 25 30
 Arg Ala Gly Val Tyr Ala Xaa Thr Xaa Asp Ala Gln Lys Xaa Ser Arg
 35 40 45
 Asn Ser Arg Glu Ala Glu Arg Trp Ile Gly Gly Met Gln Arg Gly Leu
 50 55 60
 Xaa Leu Xaa Xaa Ala Xaa Ala Ala His His Ala Leu Asp Leu Arg
 65 70 75 80
 Xaa Trp Cys Arg Ser Gly Arg Arg Ser Arg Ala Ala Xaa Gly Arg Arg
 85 90 95
 Ser Gly Arg Arg Ser Arg Arg Arg Pro Asp Pro Arg Cys Glu Ala Gly
 100 105 110
 Glu

<210> 88
<211> 111
<212> PRT
<213> Homosapiens

<220>
<223> Xaa= any amino acid
<223> Frame shift sequence
<223> Reverse strand

<400> 88
Ser Ile Thr Thr Glu Val Xaa Arg Cys Ala Leu Pro Pro Arg Val Pro
1 5 10 15
Ser Thr Thr Pro Xaa Ala Glu Tyr Gly Ser Leu Leu Ser Gln Gly Arg
20 25 30
Gln Val Cys Met Arg Xaa Leu Xaa Thr Arg Lys Ser Xaa Arg Ala Ile
35 40 45
Pro Ala Lys Leu Ser Ala Gly Leu Ala Gly Cys Ser Glu Ala Leu Xaa
50 55 60
Xaa Xaa Xaa Ala Pro Arg Thr Thr Arg Leu Ile Tyr Val Xaa Gly
65 70 75 80
Val Gly Leu Ala Ala Asp Arg Glu Gln Arg Xaa Gly Gly Gln Val
85 90 95
Asp Gly Val Asp Asp Ala Leu Ile Leu Gly Ala Arg Leu Glu Ser
100 105 110

<210> 89
<211> 256
<212> DNA
<213> Homosapiens

<220>
<221> CDS
<222> (1)...(256)
<223> N= A, T, C or G
Xaa= any amino acid

<223> Synthetically generated nucleic acid

<400> 89
gat ccg cgc atc ctc tct gtg gct ctc gcg ggg tca gag gtg gat aag 48
Asp Pro Arg Ile Leu Ser Val Ala Leu Ala Gly Ser Glu Val Asp Lys
1 5 10 15
gcc ggc cgc aag ctc gga ctt ccc gtc nca atc naa ggc ttc tgc gat 96
Ala Gly Arg Lys Leu Gly Leu Pro Val Xaa Ile Xaa Gly Phe Cys Asp
20 25 30
cnc can tac aac tac nac ggc aat ctn aca tca cgc aag atc gca ngc 144
Xaa Xaa Tyr Asn Tyr Xaa Gly Asn Leu Thr Ser Arg Lys Ile Ala Xaa
35 40 45
tcn gtc atc aag gac gcn gcg gtc ncc ncc cgg cag gtg ctc nat atn 192
Ser Val Ile Lys Asp Ala Ala Val Xaa Xaa Arg Gln Val Leu Xaa Xaa
50 55 60
gtg ttg aan aac acc atc gct cct gca acg gca aga aga tca cat gca 240
Val Leu Xaa Asn Thr Ile Ala Pro Ala Thr Ala Arg Arg Ser His Ala
65 70 75 80

agg tcc act cgc tgt g
 Arg Ser Thr Arg Cys
 85

<210> 90
<211> 85
<212> PRT
<213> Homosapiens

<220>
<223> Xaa= any amino acid
<223> Frame shift sequence

<400> 90
Asp Pro Arg Ile Leu Ser Val Ala Leu Ala Gly Ser Glu Val Asp Lys
1 5 10 15
Ala Gly Arg Lys Leu Gly Leu Pro Val Xaa Ile Xaa Gly Phe Cys Asp
20 25 30
Xaa Xaa Tyr Asn Tyr Xaa Gly Asn Leu Thr Ser Arg Lys Ile Ala Xaa
35 40 45
Ser Val Ile Lys Asp Ala Ala Val Xaa Xaa Arg Gln Val Leu Xaa Xaa
50 55 60
Val Leu Xaa Asn Thr Ile Ala Pro Ala Thr Ala Arg Arg Ser His Ala
65 70 75 80
Arg Ser Thr Arg Cys
85

<210> 91
<211> 256
<212> DNA
<213> Homosapiens

<220>
<221> CDS
<222> (2)...(256)
<223> N= A, T, C or G
Xaa= any amino acid

<223> Synthetically generated nucleic acid

<400> 91
g atc cgc gca tcc tct ctg tgg ctc tcg cg^g ggt cag agg tgg ata agg 49
Ile Arg Ala Ser Ser Leu Trp Leu Ser Arg Gly Gln Arg Trp Ile Arg
1 5 10 15
ccg gcc gca agc tcg gac ttc ccg tcn caa tcn aag gct tct gcg atc 97
Pro Ala Ala Ser Ser Asp Phe Pro Ser Gln Ser Lys Ala Ser Ala Ile
20 25 30
ncc ant aca act acn acg gca atc tna cat cac gca aga tcg can gct 145
Xaa Xaa Thr Thr Thr Ala Ile Xaa His His Ala Arg Ser Xaa Ala
35 40 45
cng tca tca agg acg cng cgg tcn ccn ccc ggc agg tgc tcn ata tng 193
Xaa Ser Ser Arg Thr Xaa Arg Ser Pro Pro Gly Arg Cys Ser Ile Xaa
50 55 60
tgt tga ana aca cca tcg ctc ctg caa cgg caa gaa gat cac atg caa 241

Cys * Xaa Thr Pro Ser Leu Leu Gln Arg Gln Glu Asp His Met Gln
 65 70 75

ggt cca ctc gct gtg 256
 Gly Pro Leu Ala Val
 80

<210> 92
 <211> 84
 <212> PRT
 <213> Homosapiens

<220>
 <223> Xaa= any amino acid

<223> Frame shift sequence

<400> 92
 Ile Arg Ala Ser Ser Leu Trp Leu Ser Arg Gly Gln Arg Trp Ile Arg
 1 5 10 15
 Pro Ala Ala Ser Ser Asp Phe Pro Ser Gln Ser Lys Ala Ser Ala Ile
 20 25 30
 Xaa Xaa Thr Thr Thr Ala Ile Xaa His His Ala Arg Ser Xaa Ala
 35 40 45
 Xaa Ser Ser Arg Thr Xaa Arg Ser Pro Pro Gly Arg Cys Ser Ile Xaa
 50 55 60
 Cys Xaa Thr Pro Ser Leu Leu Gln Arg Gln Glu Asp His Met Gln Gly
 65 70 75 80
 Pro Leu Ala Val

<210> 93
 <211> 256
 <212> DNA
 <213> Homosapiens

<220>
 <221> CDS
 <222> (3)...(256)
 <223> N= A, T, C or G
 Xaa= any amino acid

<223> Synthetically generated nucleic acid

<400> 93
 ga tcc gcg cat cct ctc tgt ggc tct cgc ggg gtc aga ggt gga taa 47
 Ser Ala His Pro Leu Cys Gly Ser Arg Gly Val Arg Gly Gly *
 1 5 10

ggc cgg ccg caa gct cg^g act tcc cgt cnc aat cna agg ctt ctg cga 95
 Gly Arg Pro Gln Ala Arg Thr Ser Arg Xaa Asn Xaa Arg Leu Arg
 15 20 25 30

tcn cca nta caa cta cna cgg caa tct nac atc acg caa gat cgc ang 143
 Ser Pro Xaa Gln Leu Xaa Arg Gln Ser Xaa Ile Thr Gln Asp Arg Xaa
 35 40 45

ctc ngt cat caa gga cgc ngc ggt cnc cnc ccg gca ggt gct cna tat 191
 Leu Xaa His Gln Gly Arg Xaa Gly Xaa Xaa Pro Ala Gly Ala Xaa Tyr
 50 55 60

ngt gtt gaa naa cac cat cgc tcc tgc aac ggc aag aag atc aca tgc 239
 Xaa Val Glu Xaa His His Arg Ser Cys Asn Gly Lys Lys Ile Thr Cys
 65 70 75

aag gtc cac tcg ctg tg
Lys Val His Ser Leu
80

<210> 94
<211> 83
<212> PRT
<213> Homosapiens

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<220>
<223> Xaa= any amino acid
<223> Frame shift sequence
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<400> 94
Ser Ala His Pro Leu Cys Gly Ser Arg Gly Val Arg Gly Gly Gly Arg
      1           5           10          15
Pro Gln Ala Arg Thr Ser Arg Xaa Asn Xaa Arg Leu Leu Arg Ser Pro
      20          25          30
Xaa Gln Leu Xaa Arg Gln Ser Xaa Ile Thr Gln Asp Arg Xaa Leu Xaa
      35          40          45
His Gln Gly Arg Xaa Gly Xaa Xaa Pro Ala Gly Ala Xaa Tyr Xaa Val
      50          55          60
Glu Xaa His His Arg Ser Cys Asn Gly Lys Lys Ile Thr Cys Lys Val
      65          70          75          80
His Ser Leu

```

<210> 95
<211> 256
<212> DNA
<213> Homosapiens

<220>
<223> N= A, T, C or G

<223> Sythetically generated nucleic acid

<223> Reverse strand

<400> 95
cacagcgagt ggaccttgca tgtgatcttc ttggccgttgc aggagcgtat gtgttttca
acacnatatn gaggcacctgc cggggngngaa ccgcggcgta ctgtatgacn gagcntgcga
tcttcgttgc tgtnagattt ccgtntgtagt tgcgtttttt atcgcagaag ccttngattt
ngacggaaag tccgagcttg cggccggcct tatccacctc tgaccggcg agagccacag
agaggatgcg cggatc

<210> 96
<211> 83
<212> PRT
<213> Homosapiens

<220>
<223> Xaa= any amino acid

<223> Frame shift sequence

<223> Reverse strand

<400> 96

His	Ser	Glu	Gln	Thr	Leu	His	Val	Ile	Phe	Leu	Pro	Leu	Gln	Glu	Arg
1				5				10					15		
Trp	Cys	Xaa	Ser	Thr	Ser	Tyr	Xaa	Ala	Pro	Ala	Gly	Xaa	Xaa	Pro	Xaa
				20				25					30		
Arg	Pro	Xaa	Ser	Xaa	Arg	Ser	Cys	Val	Met	Xaa	Asp	Cys	Arg	Xaa	Ser
				35				40				45			
Cys	Xaa	Xaa	Asp	Arg	Arg	Ser	Leu	Xaa	Leu	Xaa	Arg	Glu	Val	Arg	Ala
				50				55				60			
Cys	Gly	Arg	Pro	Tyr	Pro	Pro	Leu	Thr	Pro	Arg	Glu	Pro	Gln	Arg	Gly
				65				70				75			80
Cys	Ala	Asp													

<210> 97

<211> 82

<212> PRT

<213> Homosapiens

<220>

<223> Xaa= any amino acid

<223> Frame shift sequence

<223> Reverse strand

<400> 97

Thr	Ala	Ser	Gly	Pro	Cys	Met	Ser	Ser	Cys	Arg	Cys	Arg	Ser	Asp	Gly
1				5				10				15			
Val	Xaa	Gln	His	Xaa	Xaa	Glu	His	Leu	Pro	Xaa	Xaa	Asp	Arg	Xaa	Val
				20				25				30			
Leu	Asp	Asp	Xaa	Xaa	Cys	Asp	Leu	Ala	Cys	Xaa	Ile	Ala	Xaa	Val	Val
				35				40				45			
Val	Xaa	Xaa	Ile	Ala	Glu	Ala	Xaa	Asp	Xaa	Asp	Gly	Lys	Ser	Glu	Leu
				50				55				60			
Ala	Ala	Gly	Leu	Ile	His	Leu	Pro	Arg	Glu	Ser	His	Arg	Glu	Asp	Ala
				65				70				75			80
Arg	Ile														

<210> 98

<211> 83

<212> PRT

<213> Homosapiens

<220>

<223> Xaa= any amino acid

<223> Frame shift sequence

<223> Reverse strand

<400> 98

Gln	Arg	Val	Asp	Leu	Ala	Cys	Asp	Leu	Leu	Ala	Val	Ala	Gly	Ala	Met
1				5				10					15		
Val	Xaa	Phe	Asn	Xaa	Ile	Xaa	Ser	Thr	Cys	Arg	Xaa	Xaa	Thr	Xaa	Ala
				20				25					30		

B1
Conclude

Ser Leu Met Xaa Glu Xaa Ala Ile Leu Arg Asp Xaa Arg Leu Pro Xaa
35 40 45
Leu Xaa Trp Xaa Ser Gln Lys Pro Xaa Ile Xaa Thr Gly Ser Pro Ser
50 55 60
Leu Arg Pro Ala Leu Ser Thr Ser Asp Pro Ala Arg Ala Thr Glu Arg
65 70 75 80
Met Arg Gly